

CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 60/336,695
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 10/226,294
PRIOR FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/314,381
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/899,059
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/278,449
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 09/559,230
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/134,067
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/132,227
PRIOR FILING DATE: 1999-05-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.1
SEQ ID NO 44
LENGTH: 177
TYPE: PRT
ORGANISM: human
US-10-310-793-44

Query Match 100.0%; Score 951; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSPSWLIFIFLOLETAKEPCMA 60
DB 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSPSWLIFIFLOLETAKEPCMA 60
QY 61 KFGPLPSKQWASSEPCVNVKSDMKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120
DB 61 KFGPLPSKQWASSEPCVNVKSDMKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120
QY 121 KDMIQTLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177
DB 121 KDMIQTLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177

RESULT 6
US-10-202-062-40
Sequence 40, Application US/10202062
Publication No. US20040038349A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF ligand Family members
FILE REFERENCE: PFS59
CURRENT APPLICATION NUMBER: US/10/202,062
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO 40
LENGTH: 177
TYPE: PRT
ORGANISM: human
US-10-202-062-40

Query Match 100.0%; Score 951; DB 15; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSPSWLIFIFLOLETAKEPCMA 60
DB 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSPSWLIFIFLOLETAKEPCMA 60

DB 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSPSWLIFIFLOLETAKEPCMA 60
QY 61 KFGPLPSKQWASSEPCVNVKSDMKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120
DB 61 KFGPLPSKQWASSEPCVNVKSDMKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120
QY 121 KDMIQTLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177
DB 121 KDMIQTLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177

RESULT 7
US-09-345-790-2
Sequence 2, Application US/09345790
Patent No. US2002009198A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,790
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,227
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0470001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-345-790-2

Query Match 95.3%; Score 906; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.1e-87;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSPSWLIFIFLOLETAKEPCMAKFGPLPSK 68
DB 1 MPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSPSWLIFIFLOLETAKEPCMAKFGPLPSK 60
QY 69 WQWASSEPCVNVKSDMKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKNKDMIQTLT 128
DB 61 WQWASSEPCVNVKSDMKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKNKDMIQTLT 120
QY 129 NKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177
DB 121 NKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 169

RESULT 8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:26:56; Search time 40 Seconds
(without alignments)
425.759 Million cell updates/sec

Title: US-10-080-455-1

Perfect score: 951
Sequence: 1 MCLSHLEMPJSHSRTGAQ.....VKKNNTYWGIIILANPQFIS 177

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: PIR 79:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	8.6	1188	2	A71621 protein with 5'-3',
2	79.5	8.4	851	2	T18979 hypothetical prote
3	79.5	8.4	851	2	T51545 receptor protein k
4	78	8.2	564	2	S73405 hexosephosphate tr
5	77.5	8.1	352	2	D82442 probable peptide A
6	77.5	8.1	880	2	S49627 regulatory protein
7	77	8.1	326	1	VGXKRS glycoprotein VP7 p
8	77	8.1	326	1	VGXKRN glycoprotein VP7 p
9	77	8.1	326	1	VGXKRN glycoprotein VP7 p
10	76.5	8.0	233	2	S11688 tumor necrosis fac
11	76	8.0	209	2	A86736 hypothetical prote
12	76	8.0	525	2	E70125 MADS-box protein d
13	75.5	7.9	222	2	S51934 MHC class I protei
14	75.5	7.9	314	2	I50811 hypothetical prote
15	75.5	7.9	686	2	T20898 hypothetical prote
16	75.5	7.9	3890	2	C89921 Fp14 protein - fow
17	75	7.9	129	2	B35216 ORF MSU069 probabl
18	75	7.9	575	2	T28230 tumor necrosis fac
19	74.5	7.8	233	1	S22052 GTP-binding regula
20	74.5	7.8	355	2	A48976 probable dolichol
21	74.5	7.8	465	2	T41511 rfbL protein VC024
22	74.5	7.8	471	2	S28476 CD40 receptor-asso
23	74.5	7.8	543	2	S68467 protein K09H11.1 l
24	74.5	7.8	974	2	D83057 G protein alpha su
25	74	7.8	356	2	UC7660 CD40 receptor-asso
26	74	7.8	567	2	I49272 CD40 receptor-asso
27	74	7.8	568	2	A55960 protein T2E6.10 [I
28	74	7.8	757	2	F96518 hypothetical prote
29	73.5	7.7	345	2	E71858

30	73.5	7.7	504	2	T47446 hypothetical prote
31	73.5	7.7	609	1	A43458 replication protei
32	73.5	7.7	650	1	UC7937 transcription acti
33	73	7.7	166	2	S12723 interferon gamma p
34	73	7.7	326	1	VGXKRS glycoprotein VP7 p
35	73	7.7	326	1	VGXKRS glycoprotein VP7 p
36	73	7.7	1274	2	T40813 neurotoxin type F
37	72.5	7.6	277	2	T46209 hypothetical prote
38	72.5	7.6	442	2	T18917 probable glucan sy
39	72.5	7.6	1510	2	C84727 hypothetical prote
40	72	7.6	393	2	D75207 penicillin-binding
41	72	7.6	447	2	A02474 penicillin-binding
42	72	7.6	477	2	S32222 probable purine nu
43	72	7.6	486	2	F35965 hypothetical prote
44	72	7.6	545	2	S46151
45	72	7.6	1447	2	T15200 hypothetical prote

ALIGNMENTS

RESULT 1

A71621 protein with 5'-3', exonuclease domain (Kem-1 family) PFB0205c - malaria parasite (Plasmac protein)
C/Species: Plasmodium falciparum
C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #ext_change 09-Jul-2004
C/Accession: A71621
R/Gardner, M.J.; Tetteijn, H.; Carucci, D.J.; Cummings, L.M.; Kravind, L.; Koonin, E.V.; Perera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A/Reference number: A71600; W01D:99021743; PMID:9804551
A/Accession: A71621
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 11188 <GAR>
A/Cross-references: UNIPROT:O96143; GB:AE001380; GB:AE001362; NID:G3845120; PIDN:AACT183
A/Experimental source: clone 307
C/Genetics:
A/Gene: PFB0205c

Query Match	8.6%	Score 82;	DB 2;	Length 1188;
Best Local Similarity	30.4%	Pred. No. 19;		
Matches	38;	Conservative 11;	Mismatches 36;	Indels 40;
				Gaps 9;
OY	41	FSWIFIFLOLETAKEPCMAKFG-PLPSKQMASSEPPCV-----NKVSDW-----KIFIL 90		
Db	7	YMLIVFLFFLE-----LAKGILPGLHKW-VINNPSVCXIVDRNKLIDWNCIGKLEKA 59		
OY	91	Q-----NGLYILYGVAPNMYNDVAPFEVLYXNKMIOTLVNKS KION 135		
Db	60	KGKHKNHNGGDNNGDNNNDNNYDNNYDNNYNGCEIN-KNIRKD--NYYDN-----N 111		
OY	136	VGCTY 140		
Db	112	INNTY 116		

RESULT 2

T18979 hypothetical protein C06B3.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 09-Jul-2004
C/Accession: T18979
R/Percy, C.
Submitted to the EMBL Data Library, July 1996
A/Reference number: T18979
A/Accession: T18979
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-665 <ML>
A/Cross-references: UNIPROT:Q17701; EMBL:Z77652; PIDN:CA01113.1; GSPDB:GN00023; CESP:
A/Experimental source: clone C06B3

S49627
 regulatory protein ARGR2 - yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: protein YML099c
 C/Species: *Saccharomyces cerevisiae*
 C/Date: 02-Dec-1994 #sequence_revision 10-Feb-1995 #text_change 16-Aug-2004
 C/Accession: S49627; A25064
 R/Gentiles, S.; Bowman, S.
 submitted to the EMBL Data Library, November 1994
 A/Reference number: S49627
 A/Accession: S49627
 A/Molecule type: DNA
 A/Residues: 1-880 <GEN>
 A/Cross-references: UNIPROT:P05085; EMBL:Z46660; NID:9575702; PIDD:CAA86638.1; PID:95757
 R/Messinguy, F.; Dubois, E.; Descamps, F.
 Eur. J. Biochem. 157, 77-81, 1986
 A/Title: Nucleotide sequence of the ARGR1 regulatory gene and amino acid sequence homol
 A/Reference number: A25064; MUID:86220196; PMID:3709534
 A/Accession: A25064
 A/Molecule type: DNA
 A/Residues: 1-3,'F',5-128,130-131,'L',132-282,'V',284-344,'V',346-365,'Q',367-548,'A',55
 C/Genetics:
 A/Gene: SGD:ARG81; ARGR2
 A/Cross-references: MIPS:YML099c; SGD:S0004565
 A/Map position: 13L
 C/Superfamily: GAL4 zinc binuclear cluster homology
 C/Keywords: DNA binding; nucleus
 F/16-53/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 Query Match 8.1%; Score 77.5; DB 2; Length 880;
 Best Local Similarity 22.8%; Pred. No. 35;
 Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;
 QY 45 IFFIFLOI---ETAKPEPCMAK-----FGPLPSKQWMASEPPCVNKV----- 82
 Db 555 IEFFLKIQDSTALDKRAEIVILBSEBDNKKPLDTSNATSSSEPRVDVQEGIFRE 614
 QY 83 ----SPWK--LEILLQNGLYLIYGQVAPNA---YNDVAPFEVRLYKMKMIGTLTNKSK 132
 Db 615 ALNENDKIHIEFKEKITVNSADSPFSSTTPPIFTNIA---TESYNNKSDISKLVSKTD 671
 QY 133 IQNVGGTYELH-VGDTIDLIFNSEHQVLKNNTYGIIILANPQ 174
 Db 672 -ENIGTDSLVLGPNLSILFLPDCVRLVRHNEYNNLYLLEVP 713
 RESULT 7
 VGKRS
 glycoprotein VP7 precursor - human rotavirus A (serotype 2 strain DS1)
 N/Alternate names: outer capsid protein VP7
 C/Species: human rotavirus A
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C/Accession: E27620
 R/Green, K.Y.; Midhun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; F
 virology 161, 153-159, 1987
 A/Title: Comparison of the amino acid sequences of the major neutralization protein of A
 A/Reference number: A27620; MUID:88044489; PMID:2823458
 A/Accession: E27620
 A/Molecule type: genomic RNA
 A/Residues: 1-326 <GRE>
 A/Cross-references: UNIPROT:P11850
 C/Genetics:
 A/Map position: segment 9
 C/Superfamily: rotavirus glycoprotein VP7
 C/Keywords: coat protein; glycoprotein; transmembrane protein
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-36/Product: glycoprotein VP7 #status predicted <GPV>
 F/32-48/Region: hydrophobic #status predicted
 F/59,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 8.1%; Score 77; DB 1; Length 326;
 Best Local Similarity 22.8%; Pred. No. 12;
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 IMLFCSIVMLPLFC-----SFSWLIPIFLOLETAKEPCMAK-----FGPLPSKQW 71
 Db 10 LTLILSIILLNLYLTKITNTMDYIRFFLLILALISFVATQYGMVLPITGSLDAYYTN 69
 QY 72 ASSEPP-----CV-----NKVSPWKLEILLQNGLYLIYGQVAPNA---NYNDVAPFEV 115
 Db 70 STSGEPFLSTLCGLYPAEAKNEISDDEMENTLSQFLTRGWPIGSVYFXDYNDINTFSV 129
 QY 116 --RLYNNKMDIQTLLNKSRIQNVGTYELHVGDTIDIFNSEHQVLKNNTYGIIILANP 173
 Db 130 NPQLYCDYNNV-----LMRYDNTSELDASELADLINE-----W-----LCNP 167
 QY 174 QFTS 177
 Db 168 MDIS 171
 RESULT 8
 VGKRN
 glycoprotein VP7 precursor - human rotavirus A (serotype 2 strain HN126)
 N/Alternate names: outer capsid protein VP7
 C/Species: human rotavirus A
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C/Accession: F27620
 R/Green, K.Y.; Midhun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; F
 virology 161, 153-159, 1987
 A/Title: Comparison of the amino acid sequences of the major neutralization protein of A
 A/Reference number: A27620; MUID:88044489; PMID:2823458
 A/Accession: F27620
 A/Molecule type: genomic RNA
 A/Residues: 1-326 <GRE>
 A/Cross-references: UNIPROT:P11851
 C/Genetics:
 A/Map position: segment 9
 C/Superfamily: rotavirus glycoprotein VP7
 C/Keywords: coat protein; glycoprotein; transmembrane protein
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-36/Product: glycoprotein VP7 #status predicted <GPV>
 F/32-48/Region: hydrophobic #status predicted
 F/69,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 8.1%; Score 77; DB 1; Length 326;
 Best Local Similarity 22.8%; Pred. No. 12;
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;
 QY 26 IMLFCSIVMLPLFC-----SFSWLIPIFLOLETAKEPCMAK-----FGPLPSKQW 71
 Db 10 LTLILSIILLNLYLTKITNTMDYIRFFLLILALISFVATQYGMVLPITGSLDAYYTN 69
 QY 72 ASSEPP-----CV-----NKVSPWKLEILLQNGLYLIYGQVAPNA---NYNDVAPFEV 115
 Db 70 STSGEPFLSTLCGLYPAEAKNEISDDEMENTLSQFLTRGWPIGSVYFXDYNDINTFSV 129
 QY 116 --RLYNNKMDIQTLLNKSRIQNVGTYELHVGDTIDIFNSEHQVLKNNTYGIIILANP 173
 Db 130 NPQLYCDYNNV-----LMRYDNTSELDASELADLINE-----W-----LCNP 167
 QY 174 QFTS 177
 Db 168 MDIS 171
 RESULT 9
 VGKRN
 glycoprotein VP7 precursor - human rotavirus A
 N/Alternate names: outer capsid protein VP7
 C/Species: human rotavirus A
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C/Accession: G27620; A93520; A04134
 R/Green, K.Y.; Midhun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; F
 virology 161, 153-159, 1987
 A/Title: Comparison of the amino acid sequences of the major neutralization protein of A
 A/Reference number: A27620; MUID:88044489; PMID:2823458

```

A:Accession: G276620
A:Molecule type: genomic RNA
A:Residues: 1-326 <GRE>
A:Cross-References: UNIPROT:P04328
A:Experimental source: serotype 2 strain HUS
R:Dayall-Smith, M.L.; Holmes, I.H.
Nucleic Acids Res. 12, 3973-3982, 1984
A:Title: Sequence homology between human and animal rotavirus serotype-specific glycoprotein
A:Reference number: A93520; MUID:84221410; PMID:632848
A:Accession: A93520
A:Molecule type: DNA
A:Residues: 1-326 <DNA>
A:Cross-References: GB:X00572; NID:g61680; PTDN:CAA25236.1; PID:g61681
A:Experimental source: serotype 2 strain Hu/Australia/5/7
C:Genetics:
A:Map position: segment 9
C:Superfamily: rotavirus glycoprotein VP7
C:Keywords: coat protein, glycoprotein, transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-326/Product: glycoprotein VP7 #status predicted <GPV>
F:32-48/Region: hydrophobic #status predicted
F:69,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      8.1%, Score 77; DB 1; Length 326;
Best Local Similarity 22.8%; Pred. No. 12;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LMLFCSYMLFLC-----SFSWLFIFLQETAKPCKMAK-----FGPLPSKWM 71
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 10 LTIISILINYYILKTIINEMDYILFRLLILALISPEVRQNGYMLPIGLSDAVYTN 69

QY 72 ASSEPP-----CV-----NKYSDMKLELLQNGLYITGVAPMA---NYNDVAPPEV 115
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 70 STSGEPFLITSLCYPAEAKNEISDDEMENTLSQLFLTKMPGLGVYFKDYNIDNIFSV 129

QY 116 --RLYYKNDMLQTLTKSKIQNVGGTYELHGDITDILFENSEHQLKNNITWGIILANP 173
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 130 NPQLYCDNNV-----LWKYDNTSELDASELDILINE-----W----LCNP 167

QY 174 QFIS 177
   ||
Db 168 MDIS 171

RESULT 10
S11688
tumor necrosis factor alpha precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S11688
R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A:Title: Gene sequence of feline tumor necrosis factor alpha.
A:Reference number: S11688; MUID:91016860; PMID:2216740
A:Accession: S11688
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MCS>
A:Cross-References: UNIPROT:P19101; EMBL:X54000; NID:g1084; PTDN:CAA37948.1; PID:g295777
C:Genetics:
A:introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein, lipoprotein, myristylation, transmembrane protein
F:19-20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/DistalIde Bonds: #status predicted

Query Match      8.0%, Score 76.5; DB 2; Length 233;
Best Local Similarity 20.2%; Pred. No. 9.2;
Matches 50; Conservative 31; Mismatches 54; Indels 113; Gaps 12;

QY 7 ENMLPSHRTGAGRRSSWKMLFCSYVMLFLFCSFSWIF-----IFQLQETAKPCKMAK 61
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 15 EALPKKAGPGQSGR-----CLCLSLSFLLVAGATL-----CLLH 52

QY 62 FG-----PLPSKQMAS--SEBPCVN----- 80

Db 53 FGVITGPQREELPHGLQLINPQTLRSSSRPSDPDAHVAVNPEAEGLQRLSRANAL 112

QY 81 -----KVSWMKLEILQNGHYLYIGQV-----APNANY---NDVAFPEVRLYKKNKDMIGT 126

Db 113 LANGVELDNDQLKVPSSDGLYLYISQVLFYTGQCSPTSHVLLTHAISRFVAYSQTKVILISA 172

QY 127 LTNKSKIQN-----VGGTYELHVGDTID-----LTFNSHGYLXKN 162

Db 173 I--KSPCCRETPEGAEAKPWYEPYLGVGVEQLKGRDLSSTEINLPAYLDPAESGV---- 226

QY 163 TYWGIIIL 170

Db 227 -YFGIALL 233

RESULT 11

A86736

Hypothetical protein yjbb [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C.Species: Lactococcus lactis subsp. lactis

C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #ext_change 09-Jul-2004

C.Accession: A86736

R.BioRx, A.; Winkler, P.; Manger, S.; Tallon, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A.Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi

A.Reference number: A86625; MUID:21235186; PMID:11337471

A.Accession: A86736

A>Status: preliminary

A.Molecule type: DNA

A.Residues: 1-209 <STO>

A.Cross-references: UNIPROT:Q9CH50; GB:AE005176; PID:912723820; PIDN:AAK04987.1; GSPDB:GR

A.Experimental source: strain IL1403

C.Genetics:

A.Gene: yjbb

Query Match 8.0%; Score 76; DB 2; Length 209;

Best Local Similarity 21.0%; Pred. No. 9;

Matches 37; Conservative 26; Mismatches 69; Indels 44; Gaps 6;

QY 1 MCLSHENMPISHSRTQGAQRSSMKLWLFCSIVMLFLFCSFSLIFFLQLETAKEPCMA 60

Db 33 LALALFLFLILATRSASVLRISFIFMAIS--VMILFTYGMFWALIF----- 78

QY 61 KFGPLPSKQMASSEPPCVNKVSDMKLEILQNGL-YLYIGQVAP-----NANYDVAP 112

Db 79 -----PLTACIVFWKNNPREGKVFNSYEDISQDSSESIMNQNDDIID 122

QY 113 FEVRLYK---AKDMQTLTNKSKI---QNVGGTYELHVGDTIDLFNSEHQVKNN 162

Db 123 LDDVTFKSGNSLSIKKMTGNTKIIVPEIDVGSIDLITNAGLVKIRNEAQLNAGN 178

RESULT 12

E70125

Hypothetical protein BB0205 - Lyme disease spirochete

C.Species: Borrelia burgdorferi (Lyme disease spirochete)

C.Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #ext_change 09-Jul-2004

C.Accession: E70125

R.Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Jadhigra, R.; White,

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A.Authors: Smith, H.O.; Venter, J.C.

A.Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A.Reference number: A70100; MUID:98065943; PMID:9403685

A.Accession: E70125

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-525 <KLB>

A.Cross-references: UNIPROT:O51223; GB:AE001131; GB:AE000783; NID:92688098; PIDN:ACG6601

CC induce apoptosis in mammalian cancer cells. DNA19355 polypeptides
 CC stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-
 CC cells, and so can be used to stimulate a proinflammatory response in
 CC mammalian cells

XX Sequence 177 AA;

Query Match 100.0%; Score 951; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4.7e-97;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENNPILSHSRTOGAQRSSWKLMIFCSIVMLIFCSFSLIFIFLOETAKEPCMA 60
 Db 1 MCLSHLENNPILSHSRTOGAQRSSWKLMIFCSIVMLIFCSFSLIFIFLOETAKEPCMA 60
 QY 61 KFGPLPSKQWASSEPPCVNKKVSDWKLEILQNGLYLIYQVAPNANNVDAPEVRLYKN 120
 Db 61 KFGPLPSKQWASSEPPCVNKKVSDWKLEILQNGLYLIYQVAPNANNVDAPEVRLYKN 120
 QY 121 KDMIQTLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYWGIIILANPQFIS 177
 Db 121 KDMIQTLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYWGIIILANPQFIS 177

RESULT 2

AAV06646
 ID AAV06646 standard; protein; 177 AA.

AC AAV06646;
 DT 26-OCT-1999 (first entry)

DE Human PRO364 ligand.

KM PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;
 KM inflammation; antiinflammatory; NF-KB activation; autoimmune disease;
 KM therapy.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1..25
 FT /note= "cytoplasmic domain"
 FT 26..51
 FT /note= "transmembrane domain"
 FT 52..177
 FT /note= "extracellular domain"
 FT Modified-site 129
 FT /note= "N-glycosylation"
 FT Modified-site 161
 FT /note= "N-glycosylation"

PN WO9940196-A1.

PD 12-AUG-1999.

PF 09-FEB-1999; 99WO-US002642.

PR 09-FEB-1998; 98US-0074087P.

PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Gurney AL, Marsters SA, Pilti RM, Wood WI;
 PI Goddard A;

DR WPI; 1999-494296/41.

DR N-PSDB; AAX87726.

PT Tumour necrosis factor receptor homologue - useful for, e.g. modulating
 PT apoptosis and NF-KB activation and proinflammatory or autoimmune
 PR responses.

XX Example 2; Fig 5A; 104pp; English.

XX The present sequence represents a putative ligand for PRO364 (see also
 CC AAY06605), a novel member of the tumour necrosis factor receptor family.
 CC The sequence was deduced from an isolated cDNA clone (see AAX87726).
 CC Hydropathy analysis suggests a type II transmembrane homology. The
 CC mol. wt. is 20,308. Identity is shown to human Apo-2L (19.8%), Fas/Apo1-
 CC ligand (19.0%), TNF-alpha (20.6%) and lymphotxin-alpha (17.5%). PRO364
 CC is useful for modulating apoptosis, NF-KB activation and proinflammatory
 CC or autoimmune responses in mammalian cells

XX Sequence 177 AA;

Query Match 100.0%; Score 951; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4.7e-97;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENNPILSHSRTOGAQRSSWKLMIFCSIVMLIFCSFSLIFIFLOETAKEPCMA 60
 Db 1 MCLSHLENNPILSHSRTOGAQRSSWKLMIFCSIVMLIFCSFSLIFIFLOETAKEPCMA 60
 QY 61 KFGPLPSKQWASSEPPCVNKKVSDWKLEILQNGLYLIYQVAPNANNVDAPEVRLYKN 120
 Db 61 KFGPLPSKQWASSEPPCVNKKVSDWKLEILQNGLYLIYQVAPNANNVDAPEVRLYKN 120
 QY 121 KDMIQTLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYWGIIILANPQFIS 177
 Db 121 KDMIQTLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYWGIIILANPQFIS 177

RESULT 3

AAB47056
 ID AAB47056 standard; protein; 177 AA.

AC AAB47056;

DT 08-MAY-2001 (first entry)

DE PRO175.

KM PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
 KM hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;
 KM human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
 KM myocardial infarction; PGE 2alpha; trauma; cancer; angiogenesis;
 KM age-related macular degeneration; antibody; periodontal disease;
 KM vascular-related drug targeting; atherosclerosis; hypertension;
 KM inflammatory vasculitides; Reynaud's disease; aneurysm;
 KM arterial restenosis; thrombopilebitis; tumor angiogenesis; lung; liver;
 KM fibrosis; neuropathy; rheumatoid arthritis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..25
 FT /note= "Cytoplasmic region"
 FT 26..51
 FT /note= "Transmembrane region"
 FT Region 52..177
 FT /note= "Extracellular region"
 FT Modified-site 129
 FT /note= "N-glycosylated"
 FT Modified-site 161
 FT /note= "N-glycosylated"

PN WO200103720-A2.

PD 18-JAN-2001.

PF 11-JUL-2000; 2000WO-US018867.

PR 12-JUL-1999; 99US-0143304P.

PA (GETH) GENENTECH INC.

PI Williams PM, Gerritsen ME;
 XX
 DR WPI: 2001-13825/14.
 XX N-PSDB; AAC85435.
 XX
 PT Composition for diagnosing and treating cardiovascular, endothelial and
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
 XX
 PS Claim 2; Fig 5; 76pp; English.
 XX
 CC This sequence represents PRO175 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor ligand (HGIRL). The
 CC corresponding receptor (GIRP), PRO364, is given in AAB47054. PRO364 and
 CC PRO175 may be used in a mixture with a cardiovascular, endothelial,
 CC angiogenic or angiostatic agent for the treatment of a cardiovascular,
 CC endothelial, angiogenic or angiostatic disorder. The PRO364 sequence was
 CC isolated from an expressed sequence tag (EST) database as having homology
 CC to members of the tumor necrosis factor receptor (TNFR) family of
 CC polypeptides. The PRO175 CDNA sequence was isolated from a library of
 CC cDNA fragments derived from human umbilical vein endothelial cells
 CC (HUVEC). Administering an effective amount of PRO364 or PRO175 or their
 CC antagonists is useful for treating cardiac hypertrophy (which is
 CC initiated by myocardial infarction and characterized by the presence of
 CC an elevated level of BGP 2alpha), trauma, a cancer, or age-related
 CC macular degeneration in a human. Administering a therapeutically
 CC effective amount of an antibody that binds PRO364 or PRO175 is useful for
 CC inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering
 CC from a tumor or a retinal disorder. PRO364 or PRO175, or their
 CC antagonists, are useful for vascular-related drug targeting or as
 CC therapeutic targets for the treatment or prevention of atherosclerosis,
 CC hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,
 CC arterial stenosis, thrombophlebitis, tumor angiogenesis, gut protection
 CC or regeneration and treatment of lung or liver fibrosis, periodontal
 CC diseases, attraction of bone-forming cells, central and peripheral
 CC nervous system disease and neuropathies and rheumatoid arthritis
 XX
 SQ Sequence 177 AA:
 Query Match 100.0%; Score 951; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4.7e-97;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCLSHLEMPLSHRTGAGRSWKLFCISVWLPFCFSWLIFFLELETAKEPCMA 60
 DB 1 MCLSHLEMPLSHRTGAGRSWKLFCISVWLPFCFSWLIFFLELETAKEPCMA 60
 QY 61 KFGPLPSKQWASSEPCVKNKVDKLEIIQNGLYLYIGVAPNANTNDVAPFEVRLYKN 120
 DB 61 KFGPLPSKQWASSEPCVKNKVDKLEIIQNGLYLYIGVAPNANTNDVAPFEVRLYKN 120
 QY 121 KDMIGTLTNKSKIONVGTVEHAGDITDILFENSEHOVLKNNMTWGITILANPQFIS 177
 DB 121 KDMIGTLTNKSKIONVGTVEHAGDITDILFENSEHOVLKNNMTWGITILANPQFIS 177
 RESULT 4
 AAB20109
 ID AAB20109 standard; protein; 177 AA.
 XX
 AC AAB20109;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Human immunostimulant PRO175.
 XX
 KW PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;
 KW antirheumatic; antiinflammatory; antianemic; immunosuppressive;
 KW antihypertensive; antidiabetic; neuroprotective; hepatoprotective; virucide;
 KW dermatological; antipsoriatic; antiasthmatic; antiallergic;
 KW immunostimulant.
 XX
 OS Homo sapiens.
 XX

EH Key Location/Qualifiers
 FT Peptide 1..44
 FT /label= Signal_peptide
 FT Modified-site 18..24
 FT /note="N-myristoylation site"
 FT Protein 45..177
 FT /label= Mature_protein
 FT Modified-site 129..133
 FT /note="Asn is N-glycosylated"
 FT Modified-site 161..165
 FT /note="Asn is N-glycosylated"
 XX
 XX WO200105972-A1.
 XX
 XX 25-JAN-2001.
 XX
 XX 15-MAR-2000; 2000MO-US006884.
 XX
 XX 20-JUL-1999; 99US-0144758P.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ,
 XX Gurney AU, Hillan KJ, Mark MR, Marsters SA, Pitli RM, Tumas D,
 XX Watanabe CK, Wood WI;
 DR WPI: 2001-103149/11.
 DR N-PSDB; AAF30051.
 PS
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
 PT diagnosing and treating immune-related disorders, such as multiple
 PT sclerosis, rheumatoid arthritis and diabetes.
 XX
 XX Claim 20; Fig 4; 127pp; English.
 XX
 CC The present sequence is that of PRO175 (UNQ149), a novel human
 CC immunomodulator protein (20 kDa, pI 8.08) showing homology to tumor
 CC necrosis factor family members. The invention provides polynucleotides
 CC (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)
 CC including PRO175. Claimed compositions comprising these proteins or their
 CC agonists are useful for increasing infiltration of inflammatory cells
 CC into a tissue of a mammal, stimulating or enhancing an immune response in
 CC a mammal, or increasing the proliferation of T-lymphocytes in a mammal in
 CC response to an antigen. Claimed compositions comprising the PRO
 CC polypeptide or its antagonist have the opposite effect. A claimed method
 CC for treating an immune related disorder, such as a T cell disorder,
 CC involves administering the PRO polypeptide, an agonist antibody or an
 CC antagonist antibody. The disorder is selected from systemic lupus
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,
 CC thyroditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinated diseases (such as multiple sclerosis), autoimmune chronic
 CC active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,
 CC sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis
 CC and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,
 CC (auto)immune-mediated skin diseases (such as bullous skin disease,
 CC erythema multiforme and psoriasis), allergic diseases (such as asthma,
 CC allergic rhinitis, atopic dermatitis, food hypersensitivity and
 CC urticaria), immunologic diseases of the lung and transplantation
 CC associated diseases (such as graft rejection and graft-versus-host
 CC disease) (all claimed). Claimed methods of diagnosing these disorders
 CC comprise detecting the level of expression of the PRO gene. Also claimed
 CC are a method of identifying a compound capable of inhibiting the
 CC expression or activity of the PRO polypeptide, vectors, host cells,
 CC antibodies, and a method of stimulating an immune response in a mammal
 CC using PRO179
 XX
 SQ Sequence 177 AA:
 Query Match 100.0%; Score 951; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4.7e-97;

Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPLESHSTQGAQRSSMKLMFCSTVMLFLFCSSFWLFIPLQETAKEPCMA 60
 DB 1 MCLSHLEMPLESHSTQGAQRSSMKLMFCSTVMLFLFCSSFWLFIPLQETAKEPCMA 60
 QY 61 KFGPLPSKQWASSSEPPCVNKNVSDMKLEILLQNGYLIIYQVAPNANNYDVAFEEVRLYKN 120
 DB 61 KFGPLPSKQWASSSEPPCVNKNVSDMKLEILLQNGYLIIYQVAPNANNYDVAFEEVRLYKN 120
 QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSEHQV LKNNTWGIIILANPQFIS 177
 DB 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSEHQV LKNNTWGIIILANPQFIS 177

RESULT 5
 AAB53065
 ID AAB53065 standard; protein, 177 AA.
 XX AAB53065;
 AC
 XX 28-FEB-2001 (first entry)
 DT
 XX Human angiogenesis-associated protein PRO175, SEQ ID NO:9.
 DE Human angiogenesis-associated protein; PRO: endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 EN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 PF 05-JAN-2000; 2000WO-US000219.
 XX
 XX 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144738P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Garber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Masters SA;
 PI Paoni NF, Pletti RM, Watanabe CK, Williams PM, Wood WJ;
 XX WPI, 2001-090793/10.
 DR N-PSDB; AAC97374.
 XX
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic
 PT disorders, such as atherosclerosis, wounds or cancer.
 XX
 PS Claim 69; Fig 4; 293pp; English.
 XX

CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to screen
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals
 CC useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a PRO protein of the invention
 XX

SEQ Sequence 177 AA;

Query Match 100.0%; Score 951; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4,7e-97;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPLESHSTQGAQRSSMKLMFCSTVMLFLFCSSFWLFIPLQETAKEPCMA 60
 DB 1 MCLSHLEMPLESHSTQGAQRSSMKLMFCSTVMLFLFCSSFWLFIPLQETAKEPCMA 60
 QY 61 KFGPLPSKQWASSSEPPCVNKNVSDMKLEILLQNGYLIIYQVAPNANNYDVAFEEVRLYKN 120
 DB 61 KFGPLPSKQWASSSEPPCVNKNVSDMKLEILLQNGYLIIYQVAPNANNYDVAFEEVRLYKN 120
 QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSEHQV LKNNTWGIIILANPQFIS 177
 DB 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSEHQV LKNNTWGIIILANPQFIS 177

RESULT 6
 AAB47287
 ID AAB47287 standard; protein, 177 AA.
 XX
 AC AAB47287;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 XX PRO175 polypeptide.
 DE
 XX
 XX PRO: type II transmembrane protein; tumour necrosis factor; stroke;
 KW heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;
 KW myocardial infarction; cardiac hypertrophy; Pgf_2alpha; trauma; bone;
 KW cancer; age-related macular degeneration; wound; burn; hypertension;
 KW diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; amyloidotic lateral sclerosis;
 KW endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..25
 PS

Query Match	100.0%	Score 951;	DB 4;	Length 177;
Best Local Similarity	100.0%;	Pred. No. 4.7e-97;		
Matches 177; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	61	KRPGLPSKQMASSPEPCNKRISDWKLEILONGLYLTYGVAPNANNDVAPEFVRLYKN	120
Db	61	KRPGLPSKQMASSPEPCNKRISDWKLEILONGLYLTYGVAPNANNDVAPEFVRLYKN	120
Qy	121	KDMIQTLTKSKRIQNVGTFYELVAGDTLDLFPNSEHVLKNNITYWGIIILANPOEIS	177
Db	121	KDMIQTLTKSKRIQNVGTFYELVAGDTLDLFPNSEHVLKNNITYWGIIILANPOEIS	177
RESULT 7			
ID	AAB50979	standard; protein; 177 AA.	
XX			
AC	AAB50979;		
XX			
DT	21-MAR-2001	(first entry)	
XX			
DE	Human PRO175 protein.		
XX			
KW	Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;		
KW	vasotrophic; antineuralgic; antiarthritic; antiinflammatory; cytostatic;		
KW	vulnerable; antiautagenic; gene therapy; cardiovascular disease;		
KW	endothelial disorder; angiogenic disorder; cancer; periodontal disease;		
KW	wound healing.		
XX			
XX	Homo sapiens.		
XX			
PN	WO200073445-A2.		
XX			
PD	07-DEC-2000.		
XX			
FF	17-MAY-2000; 2000MO-US013705.		
XX			
PR	02-JUN-1999; 99MO-US012252.		
PR	23-JUN-1999; 99US-01410376.		
PR	20-JUL-1999; 99US-0144758P.		
PR	26-JUL-1999; 99US-0145698P.		
PR	28-JUL-1999; 99US-0146222P.		
PR	01-SEP-1999; 99MO-US020111.		
PR	30-NOV-1999; 99MO-US028313.		
PR	30-NOV-1999; 99MO-US028409.		
PR	02-DEC-1999; 99MO-US028565.		
PR	16-DEC-1999; 99MO-US030095.		
PR	05-JAN-2000; 2000MO-US000219.		
PR	06-JAN-2000; 2000MO-US000376.		
PR	11-FEB-2000; 2000MO-US003565.		
PR	18-FEB-2000; 2000MO-US004341.		
PR	18-FEB-2000; 2000MO-US004342.		
PR	24-FEB-2000; 2000MO-US005004.		
PR	02-MAR-2000; 2000MO-US005841.		
PR	10-MAR-2000; 2000MO-US006319.		
PR	15-MAR-2000; 2000MO-US006884.		
PR	21-MAR-2000; 2000MO-US007532.		
PR	30-MAR-2000; 2000MO-US008439.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;		
PI	Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;		
PI	Paoni NF, Pilti RM, Watanabe CK, Williams PM, Wood WI;		
XX			
DR	WPI: 2001-025251/03.		
DR	N-PSDB; AAC90563.		
XX			
PT	Seventeen nucleic acids encoding PRO polypeptides which are useful in		
PT	diagnosis and treatment of cardiovascular, endothelial or angiogenic		
PT	disorders in a mammal.		
XX			
PS	Claim 71; Fig 2; 182pp; English.		
XX			
CC	The present sequence is one of seventeen novel PRO polypeptides. The PRO		
CC	nucleic acids, polypeptides, agonists and antagonists are useful for		

CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial
 CC retinosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and
 CC antagonists are also used to prevent tumour angiogenesis and for treating
 CC periodontal diseases. They are also used to stimulate wound healing and
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder

SQ Sequence 177 AA;

Query Match 100.0%; Score 951; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4.7e-97;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPISHRTQAGRSSWKMLFCSTIVMLLFICSFSLIFFLQETAKEPCMA 60
 DB 1 MCLSHLEMPISHRTQAGRSSWKMLFCSTIVMLLFICSFSLIFFLQETAKEPCMA 60

QY 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLNGGLIYGVAPNANYNDVAPFEVRLYKN 120
 DB 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLNGGLIYGVAPNANYNDVAPFEVRLYKN 120

QY 121 KDMIGTLTNKSKIONVGTYELHVGDTIDLI FNSHQVLKNNYWGIIILANPQFIS 177
 DB 121 KDMIGTLTNKSKIONVGTYELHVGDTIDLI FNSHQVLKNNYWGIIILANPQFIS 177

RESULT 8
 ID AUA81953 standard; protein; 177 AA.
 AC AUA81953;
 DT 09-APR-2002 (first entry)
 XX Human PRO175.
 XX Human PRO175.

KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;
 KW retinal cell injury; ocular disease; retinitis pigmentosa;
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;
 KW retinal degenerative disease; macular hole; degenerative myopia;
 KW acute retinal necrosis syndrome; traumatic chorioretinopathy;
 KW Putscher's retinopathy; oedema; ischaemic condition;
 KW retinal vision occlusion; collagen vascular disease;
 KW thrombocytopenic purpura, uveitis; retinal vasculitis; Eales disease;
 KW systemic lupus erythematosus; environmental trauma.

OS Homo sapiens.
 XX WO200109327-A2.
 XX 08-FEB-2001.
 XX 28-JUL-2000; 2000WO-US020710.
 XX 28-JUL-1999; 99US-0146222P.
 XX 13-SEP-1999; 99WO-US020944.
 XX 15-SEP-1999; 99WO-US021090.
 XX 29-NOV-1999; 99WO-US028214.
 XX 30-NOV-1999; 99WO-US028313.
 XX 01-DEC-1999; 99WO-US028301.
 XX 05-JAN-2000; 2000WO-US000219.
 XX 06-JAN-2000; 2000WO-US000376.
 XX 11-FEB-2000; 2000WO-US003565.
 XX 18-FEB-2000; 2000WO-US004341.
 XX 22-FEB-2000; 2000WO-US004414.
 XX 24-FEB-2000; 2000WO-US005004.
 XX 02-MAR-2000; 2000WO-US005841.
 XX 15-MAR-2000; 2000WO-US006884.
 XX 30-MAR-2000; 2000WO-US008439.
 XX 17-MAY-2000; 2000WO-US013705.

XX (GEN) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;
 XX Kljavin JI, Lafleur M, Mark MR, Marsters SA, Pfitz RM, Watanabe CK,
 PI Wood WJ;
 XX MPI: 2002-130120/17.
 DR N-PEDB; ABK28562.
 XX Promoting survival of retinal cells, or delaying or preventing retinal
 PT cell injury or death, by contacting retinal cells with PRO175, 220, 216,
 PR 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132 polypeptide.
 PS Claim 44; Fig 2; 152pp; English.

XX The invention relates to promoting the survival of retinal cells, or
 CC delaying or preventing retinal cell injury or death, by contacting the
 CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,
 CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,
 CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids
 CC encoding the PRO proteins, a vector comprising the nucleic acid, a host
 CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are
 CC useful for promoting survival of retinal cells (retinal neurons such as
 CC retinal ganglion cells, displaced retinal ganglion cells, amacrine cells,
 CC displaced amacrine cells, horizontal neurons or bipolar neurons, rod
 CC photoreceptors, or supportive cells such as Muller cells or pigment
 CC epithelial cells), or delaying or preventing retinal cell injury or death
 CC caused by ocular disease (which is or is associated with retinitis
 CC pigmentosa, macular degeneration, retinal detachment, retinal tear,
 CC retinopathy, retinal degenerative disease, macular hole, degenerative
 CC myopia, acute retinal necrosis syndrome, traumatic chorioretinopathy or
 CC contusion, Putscher's retinopathy, oedema, an ischaemic condition,
 CC central or branch retinal vision occlusion, collagen vascular disease,
 CC thrombocytopenic purpura, uveitis, retinal vasculitis, occlusion
 CC associated with Eales disease or systemic lupus erythematosus), retinal
 CC injury or environmental trauma. The retinal cell injury or death is
 CC delayed or prevented by substantially not causing angiogenesis or
 CC mitogenesis. The present sequence represents a PRO protein

SQ Sequence 177 AA;

Query Match 100.0%; Score 951; DB 5; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4.7e-97;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPISHRTQAGRSSWKMLFCSTIVMLLFICSFSLIFFLQETAKEPCMA 60
 DB 1 MCLSHLEMPISHRTQAGRSSWKMLFCSTIVMLLFICSFSLIFFLQETAKEPCMA 60

QY 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLNGGLIYGVAPNANYNDVAPFEVRLYKN 120
 DB 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLNGGLIYGVAPNANYNDVAPFEVRLYKN 120

QY 121 KDMIGTLTNKSKIONVGTYELHVGDTIDLI FNSHQVLKNNYWGIIILANPQFIS 177
 DB 121 KDMIGTLTNKSKIONVGTYELHVGDTIDLI FNSHQVLKNNYWGIIILANPQFIS 177

RESULT 9
 ID ABR42323 standard; protein; 177 AA.
 AC ABR42323;
 DT 11-AUG-2003 (first entry)
 XX Human GTRRL protein.
 XX Human GTRRL protein.
 XX Human; GTRRL; tumour necrosis factor; ligand; cytostatic;
 XX immunomodulator; osteopathic.
 OS Homo sapiens.

DT 18-DEC-2003 (first entry)
XX
DE Human TNF ligand family member #20.
XX
KW human; tumour necrosis factor; TNF ligand; endokine alpha;
KM excessive bone resorption disorder; osteoporosis; Paget's disease;
XX arterial calcification.
XX
OS Homo sapiens.
XX
EN US2003100074-A1.
XX
PD 29-MAY-2003.
XX
PF 15-AUG-2002; 2002US-00218547.
XX
PR 16-AUG-2001; 2001US-0312542P.
PR 30-OCT-2001; 2001US-0330761P.
XX
PA (YUGG/) YU G.
PA (NLTJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (NARD/) NARDELLI B.
XX
PI YU G, NI J, ROSEN CA, NARDELLI B;
XX
XX MPI; 2003-696072/66.
DR N-PSDB; ADC35221.
XX
XX
PT New Endokine alpha gene useful for preparing a composition for treating a
PT disease associated with excessive or insufficient bone resorption e.g.,
PT osteoporosis, Paget's disease or arterial calcification.
XX
PS Claim 1; SEQ ID NO 40; 145PP; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC tumour necrosis factor family ligand. A composition comprising the
CC isolated antibody or its fragment is used for treating an individual in
CC need of decreased level of endokine alpha activity. The endokine alpha
CC polypeptide present in a heterotrimeric complex is used for treating an
CC individual having a disorder associated with excessive bone resorption,
CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
CC individual having a disorder associated with insufficient bone resorption
CC comprises administering an endokine alpha antagonist, which is the
CC antibody that binds specifically to endokine alpha polypeptide. The
CC present sequence represents the amino acid sequence of a tumour necrosis
CC factor family ligand.
XX
SQ Sequence 177 AA;
XX
Query Match 100.0%; Score 951; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.7e-97;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MCLSHLENMPLSHSRTQGAQRSSWKLWLFCSIVMLFLCFSFWLFIPLQJETAKEPCMA 60
DB 1 MCLSHLENMPLSHSRTQGAQRSSWKLWLFCSIVMLFLCFSFWLFIPLQJETAKEPCMA 60
XX
QY 61 KFGPLPSKQWASSSEPPCVNVKVSMDKLEILLONGYLITIGQVAPNANNYDVAPFEVRLTKN 120
DB 61 KFGPLPSKQWASSSEPPCVNVKVSMDKLEILLONGYLITIGQVAPNANNYDVAPFEVRLTKN 120
XX
QY 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHQVLYKNNTYWGIIILANPQFIS 177
DB 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHQVLYKNNTYWGIIILANPQFIS 177
XX
RESULT 12
ABW02285
ID ABW02285 standard; protein; 177 AA.
XX
AC ABW02285;
XX

DT 12-FEB-2004 (first entry)
XX
DE Human endokine alpha protein.
XX
KW Gastrointestinal tract disorder; tumour necrosis factor; TNF; DR3; TR6;
KM TNF-gamma-beta protein; inflammatory bowel disease; Crohn's disease;
XX ulcerative colitis; endokine alpha protein; human.
XX
OS Homo sapiens.
XX
EN US2003198640-A1.
XX
PD 23-OCT-2003.
XX
PF 06-DEC-2002; 2002US-00310793.
XX
PR 07-NOV-1994; 94WO-US012880.
PR 05-JUN-1995; 95US-00461246.
PR 09-JAN-1998; 98US-00005020.
PR 09-FEB-1998; 98US-0074047P.
PR 07-AUG-1998; 98US-00131237.
PR 08-FEB-1999; 99US-00246129.
PR 30-APR-1999; 99US-0131963P.
PR 03-MAY-1999; 99US-0132227P.
PR 13-MAY-1999; 99US-0134067P.
PR 08-FEB-2000; 2000US-0180908P.
PR 27-APR-2000; 2000US-00559290.
PR 07-JUL-2000; 2000US-0216879P.
PR 26-MAR-2001; 2001US-0278449P.
PR 06-JUL-2001; 2001US-00899059.
PR 24-AUG-2001; 2001US-0314381P.
PR 07-DEC-2001; 2001US-0336695P.
PR 23-AUG-2002; 2002US-00226294.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
PI YU G, NI J, ROSEN CA, ZHANG J, WEI P;
XX
XX MPI; 2003-852773/79.
DR N-PSDB; AAD63921.
XX
XX Use of tumor necrosis factor gamma-beta antagonists for treating or
PT ameliorating a disease or disorders of the gastrointestinal tract, e.g.
PT inflammatory bowel disease, Crohn's disease or ulcerative colitis.
XX
XX Disclosure; Page 153-154; 0pp; English.
XX
XX
XX The invention relates to methods and compositions for treating or
CC ameliorating a disease or disorder of the gastrointestinal tract. The
CC method involves administering a composition comprising tumour necrosis
CC factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with,
CC or suspected of having the disease or disorder. The antagonist of TNF-
CC gamma-beta is useful for treating or ameliorating a gastrointestinal
CC tract disease or disorder, specifically an inflammatory bowel disease,
CC e.g. Crohn's disease or ulcerative colitis. The present sequence is human
CC endokine alpha protein. This sequence is used to illustrate the method of
CC the invention.
XX
SQ Sequence 177 AA;
XX
Query Match 100.0%; Score 951; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.7e-97;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MCLSHLENMPLSHSRTQGAQRSSWKLWLFCSIVMLFLCFSFWLFIPLQJETAKEPCMA 60
DB 1 MCLSHLENMPLSHSRTQGAQRSSWKLWLFCSIVMLFLCFSFWLFIPLQJETAKEPCMA 60
XX
QY 61 KFGPLPSKQWASSSEPPCVNVKVSMDKLEILLONGYLITIGQVAPNANNYDVAPFEVRLTKN 120
DB 61 KFGPLPSKQWASSSEPPCVNVKVSMDKLEILLONGYLITIGQVAPNANNYDVAPFEVRLTKN 120
XX
QY 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHQVLYKNNTYWGIIILANPQFIS 177

Db 121 KMWIQLTKSKSKQNGTVELHVGDTIDLFNSEHQVLKNNYWGIIILANPQFIS 177

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RESULT 13
AAW37847
ID AAW37847 standard; protein; 169 AA.
XX
XX AAW37847;
AC
XX
XX 28-AUG-1998 (first entry)
DT
XX
XX Human endokine-alpha.
DE
XX Endokine-alpha: cytokine; tumour necrosis factor; human;
KW immunomodulation; infection; cell proliferation; angiogenesis; tumour;
KW metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;
XX diagnosis; therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..17
FT /note= "intracellular domain"
FT 18..43
FT Domain /note= "transmembrane domain"
FT /note= "extracellular domain"
FT Domain /note= "extracellular domain"
FT Peptide 44..158
FT /note= "epitope-bearing fragment (Claim 13)"
FT 44..158
FT /note= "epitope-bearing fragment (Claim 13)"
FT 57..68
FT /note= "epitope-bearing fragment (Claim 13)"
FT Peptide 69..78
FT /note= "epitope-bearing fragment (Claim 13)"
FT 94..105
FT /note= "epitope-bearing fragment (Claim 13)"
FT 108..132
FT /note= "epitope-bearing fragment (Claim 13)"
FT Peptide 142..158
FT /note= "epitope-bearing fragment (Claim 13)"
FT Peptide
PN MO9807880-A1.
XX
XX 26-FEB-1998.
PD
XX 16-AUG-1996; 96WO-US013282.
XX PF
XX 16-AUG-1996; 96WO-US013282.
XX PR
XX 16-AUG-1996; 96WO-US013282.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Yu G, Ni J, Rosen CA;
PI
XX
XX WPI; 1998-169182/15.
DR N-PSDB; AAV19195.
XX
XX Nucleic acid encoding human endokine-alpha - useful for diagnosis and
PT treatment of tumour necrosis factor-related diseases.
PT
XX
XX Claim 1; Fig 1A-B; 78pp; English.
PS
XX
XX This polypeptide comprises human endokine-alpha, a novel member of the
CC tumour necrosis factor (TNF) family of cytokines that shows 30%
CC similarity and 22% identity to human TNF-alpha. Its amino acid sequence
CC was deduced from a human striatum cDNA clone (see AAV19195). Isolation of
CC this nucleic acid allows production of recombinant endokine-alpha
CC polypeptides in transformed host cells. Endokine-alpha may be involved in
CC disorders of immunomodulation, infection, cell proliferation,
CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxaemia, and
CC may be useful for treating melanoma and sarcoma, particularly where
CC coupled to a radioisotope or cytostatic agent. Antibodies raised against

```

CC endokine-alpha are useful diagnostically and for treatment of TNF-
CC associated disease
XX
XX Sequence 169 AA:

Query Match 95.3%; Score 906; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 4.4e-92;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 9 MPLSHSRTOGAQRSSWKMLFCSYVWLFLFCSTSMILFTFLQETAKEPEPMARFGPLPSK 68
DB 1 MPLSHSRTOGAQRSSWKMLFCSYVWLFLFCSTSMILFTFLQETAKEPEPMARFGPLPSK 60
QY 69 WQWASSEPPCVNKSVMKLEILLONGLYLYGQVAPNANVNDVAPFEVRLYKXNDMTQTLT 128
DB 61 WQWASSEPPCVNKSVMKLEILLONGLYLYGQVAPNANVNDVAPFEVRLYKXNDMTQTLT 120
QY 129 NRSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILANPQFIS 177
DB 121 NRSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILANPQFIS 169

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RESULT 14
AAB08785
ID AAB08785 standard; protein; 169 AA.
XX
XX AAB08785;
AC
XX
XX 02-JAN-2001 (first entry)
DT
XX
XX A human endokine-alpha polypeptide.
DE
XX
XX Human; endokine-alpha: cytokine; tumour necrosis factor; TNF; AIDS;
KW chronic lymphocyte disorder; tumour; parasitic disease; arthritis;
KW autoimmune disease; lupus; multiple sclerosis; chronic inflammation;
KW acute inflammation; acute allograft rejection; graft versus host disease;
KW transplant rejection; foetal resorption; faecal peritonitis; allergy;
KW bowel disease; sepsis; leukaemia; chronic hypergammaglobulinaemia;
KW polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;
KW chronic active hepatitis; thyrotoxicosis; psoriasis; vitiligo;
KW Steven-Johnson syndrome; idiopathic spine; gluten-sensitive enteropathy;
KW pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;
KW discoid lupus; dense deposit disease; endocrine ophthalmopathy;
KW irritable bowel disease; asthma; Grave's disease; sarcoidosis; cataracts;
KW juvenile diabetes; insulin dependent diabetes mellitus; uveitis;
KW lymphopneumonia; polyarteritis nodosa; Sjogren's syndrome; Bechet's disease;
KW primary myxedema; polymyositis; mixed connective tissue disease;
KW keratoconjunctivitis sicca; vernal Keratoconjunctivitis; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH Domain 1..17
FT /note= "intracellular domain"
FT 18..43
FT Domain /note= "transmembrane domain"
FT /note= "extracellular domain"
FT Domain

```

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XX WO200050620-A2.
XX
XX 31-AUG-2000.
PD
XX
XX 25-FEB-2000; 2000MO-US004722.
PF
XX 26-FEB-1999; 99US-0122099P.
XX PR
XX 28-MAY-1999; 99US-0136788P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Yu G, Ni J, Rosen CA;
PI
XX
XX WPI; 2000-572097/53.
DR

```

DR N-PSDB; AAA74936.

XX Polynucleotide encoding endokine alpha protein, which is a member of
PT tumor necrosis factor useful for treating inflammatory diseases,
PT disorders such as cancer, allergy, diabetes and various neurological
PT disorders.

PS Claim 16; Fig 1; 263pp; English.

XX The present sequence represents a human endokine-alpha polypeptide. The
CC polypeptide is a cytokine which is similar to tumour necrosis factor
CC (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
CC treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
CC autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
CC inflammation, acute inflammation, acute allograft rejection, graft versus
CC host disease, transplant rejection, foetal resorption, faecal
CC peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
CC granulomatosis, dermatomyositis, scleroderma, Wegener
CC granulomatosis, Steven-Johnson syndrome, idiopathic sprue, vitiligo,
CC gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
CC bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
CC ophthalmopathy, irritable bowel disease, asthma, Grave's disease,
CC sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
CC mellitus, uveitis, lymphopenias, polyarteritis nodosa, Sjogren's
CC syndrome, Becker's disease, primary myxedema, polymyositis, mixed
CC connective tissue disease, keratoconjunctivitis sicca, and vernal
CC keratoconjunctivitis.

XX Sequence 169 AA;

Query Match 95.3%; Score 906; DB 3; Length 169;

Best Local Similarity 100.0%; Pred. No. 4.4e-99; Mismatches 0; Indels 0; Gaps 0;

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFFLQLETAKEPCMAKFGPLPSK 68
DB 1 MPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFFLQLETAKEPCMAKFGPLPSK 60

QY 69 WOMASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 128
DB 61 WOMASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 120

QY 129 NKSRIQNVGTYELHVGDTIDLIENSEHQVLKNNTYWGIILLANQFIS 177
DB 121 NKSRIQNVGTYELHVGDTIDLIENSEHQVLKNNTYWGIILLANQFIS 169

RESULT 15

AA53061
ID AA53061 standard; protein; 169 AA.

XX AA53061;

XX 03-APR-2000 (first entry)

XX Human endokine alpha protein SEQ ID NO:2.

XX Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
XX Immunomodulation; inflammation; cell proliferation; angiogenesis;
XX Tumour metastasis; apoptosis; sepsis; endotoxemia.

XX Homo sapiens.

XX US5998171-A.

XX 07-DEC-1999.

XX 15-AUG-1997; 97US-00912227.

XX 16-AUG-1996; 96US-0024058P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Rosen CA, Yu G;

XX WPI; 2000-104608/09.

DR N-PSDB; AA257314.

PT Isolated human endokine alpha gene useful as a diagnostic probes and
PT primers.

PS Claim 1; Fig 1; 31pp; English.

XX The present sequence represents human endokine alpha which is a member of
CC the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
CC protein and polynucleotides can be used in diagnostic and therapeutic
CC methods concerning TNF family-related disorders. These include disorders
CC associated with immunomodulation and inflammation, cell proliferation,
CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia

XX Sequence 169 AA;

Query Match 95.3%; Score 906; DB 3; Length 169;

Best Local Similarity 100.0%; Pred. No. 4.4e-92; Mismatches 0; Indels 0; Gaps 0;

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFFLQLETAKEPCMAKFGPLPSK 60

QY 69 WOMASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 128
DB 61 WOMASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 120

QY 129 NKSRIQNVGTYELHVGDTIDLIENSEHQVLKNNTYWGIILLANQFIS 177
DB 121 NKSRIQNVGTYELHVGDTIDLIENSEHQVLKNNTYWGIILLANQFIS 169

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:41:06 ; Search time 129 Seconds
(without alignments)
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Title: US-10-080-455-1

Perfect score: 951

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Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

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Maximum DB seq length: 200000000

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	951	100.0	177	14	US-10-218-547-40
5	951	100.0	177	14	US-10-310-793-44
6	951	100.0	177	15	US-10-202-062-40
7	906	95.3	169	9	US-09-345-790-2
8	906	95.3	169	13	US-10-136-511-2
9	608	63.9	113	14	US-10-338-083-17
10	608	63.9	113	16	US-10-611-399-17
11	281	29.5	52	9	US-09-864-761-48455
12	85.5	9.0	377	14	US-10-295-027-280
13	79.5	8.4	246	15	US-10-424-599-201262

14	79.5	8.4	879	15	US-10-149-310-52	Sequence 52, Appl
15	77.5	8.1	880	15	US-10-149-310-50	Sequence 50, Appl
16	76.5	8.0	1138	14	US-10-261-482-4	Sequence 4, Appl
17	76	8.0	1133	16	US-10-437-963-149870	Sequence 149870,
18	75.5	7.9	365	15	US-10-425-114-47601	Sequence 47601, A
19	75.5	7.9	885	16	US-10-432-171-12	Sequence 12, Appl
20	75.5	7.9	5795	9	US-09-815-242-12610	Sequence 12610, A
21	74.5	7.8	271	14	US-10-224-880C-33	Sequence 33, Appl
22	74.5	7.8	332	14	US-10-182-960-13	Sequence 13, Appl
23	74.5	7.8	543	9	US-09-157-041-2	Sequence 2, Appl
24	74.5	7.8	543	14	US-10-004-378A-35	Sequence 35, Appl
25	74.5	7.8	939	14	US-10-369-493-3816	Sequence 3816, Ap
26	74	7.8	399	15	US-10-424-599-225192	Sequence 225192,
27	74	7.8	566	8	US-08-813-323A-1	Sequence 1, Appl
28	74	7.8	567	14	US-10-247-212-7	Sequence 7, Appl
29	74	7.8	567	14	US-10-207-655-103	Sequence 103, App
30	74	7.8	568	8	US-08-813-323A-2	Sequence 2, Appl
31	74	7.8	568	14	US-10-116-275-173	Sequence 173, App
32	74	7.8	568	14	US-10-004-378A-36	Sequence 36, Appl
33	74	7.8	568	15	US-10-042-865-166	Sequence 166, App
34	74	7.8	819	16	US-10-437-963-184313	Sequence 184313,
35	74	7.8	1326	16	US-10-437-963-129340	Sequence 129340,
36	73.5	7.7	345	15	US-10-335-977-6130	Sequence 6130, Ap
37	73.5	7.7	346	15	US-10-335-977-6131	Sequence 6131, Ap
38	73.5	7.7	609	14	US-10-372-686-6	Sequence 6, Appl
39	73.5	7.7	609	14	US-10-371-558-6	Sequence 6, Appl
40	73.5	7.7	609	14	US-10-375-553-6	Sequence 6, Appl
41	73.5	7.7	609	15	US-10-372-553-6	Sequence 6, Appl
42	73.5	7.7	1419	16	US-10-437-963-125464	Sequence 125464,
43	73	7.7	249	15	US-10-335-977-6129	Sequence 6129, Ap
44	73	7.7	313	15	US-10-424-599-221929	Sequence 221929,
45	73	7.7	389	9	US-09-767-041-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-10-080-455-1
; Sequence 1, Application US/10080455
; Publication No. US20020146389A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pletli, Robert M.
; TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
; FILE REFERENCE: P150R2
; CURRENT APPLICATION NUMBER: US/10/080,455
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/195,368
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: US 60/069,661
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/065,635
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-455-1

Query Match 100.0%; Score 951; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MCLSHLENNPLSHRTOGAORSSWKMLPFCSTYMLFLCFSWLFPIQLTAKRCMA 60
DB 1 MCLSHLENNPLSHRTOGAORSSWKMLPFCSTYMLFLCFSWLFPIQLTAKRCMA 60

QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
Db 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177
Db 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177

RESULT 2
US-10-116-378-16
; Sequence 16, Application US/10116378
; Publication No. US2002015093A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Masters, Scott A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 16
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-16

Query Match 100.0%; Score 951; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSTVMLLFLCSPSWLIFIFLOJETAKEPCMA 60
Db 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSTVMLLFLCSPSWLIFIFLOJETAKEPCMA 60
QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
Db 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177
Db 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177

RESULT 3
US-10-151-882-39
; Sequence 39, Application US/10151882
; Publication No. US20030053862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-151-882-39

Query Match 100.0%; Score 951; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSTVMLLFLCSPSWLIFIFLOJETAKEPCMA 60
Db 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSTVMLLFLCSPSWLIFIFLOJETAKEPCMA 60
QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
Db 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177
Db 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177

RESULT 4
US-10-218-547-40
; Sequence 40, Application US/10218547
; Publication No. US20030100074A1

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 177
; TYPE: PRT
; ORGANISM: human
US-10-218-547-40

Query Match 100.0%; Score 951; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSTVMLLFLCSPSWLIFIFLOJETAKEPCMA 60
Db 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCSTVMLLFLCSPSWLIFIFLOJETAKEPCMA 60
QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
Db 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLIYGQVAPNANNVDVAPFEVRLYKN 120
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177
Db 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177

RESULT 5
US-10-310-793-44
; Sequence 44, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Bing
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793

```

; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 177
; TYPE: PRT
; ORGANISM: human
US-10-310-793-44
```

```

Query Match          100.0%; Score 951; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 MCISHENMPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFLQLETAKEPCMA 60
    |||
DB 1 MCISHENMPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFLQLETAKEPCMA 60
    |||
QY 61 KFGPLPSKQWMASSPPCVNKSVDWKLELLQNGLYLYIGVAPNANNDVAPFEVRLYKN 120
    |||
DB 61 KFGPLPSKQWMASSPPCVNKSVDWKLELLQNGLYLYIGVAPNANNDVAPFEVRLYKN 120
    |||
QY 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILANPQFIS 177
    |||
DB 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILANPQFIS 177
    |||
```

```

RESULT 6
US-10-202-062-40
; Sequence 40, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 177
; TYPE: PRT
; ORGANISM: human
US-10-202-062-40
```

```

Query Match          100.0%; Score 951; DB 15; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCISHENMPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFLQLETAKEPCMA 60
    |||
```

```

DB 1 MCISHENMPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFLQLETAKEPCMA 60
    |||
QY 61 KFGPLPSKQWMASSPPCVNKSVDWKLELLQNGLYLYIGVAPNANNDVAPFEVRLYKN 120
    |||
DB 61 KFGPLPSKQWMASSPPCVNKSVDWKLELLQNGLYLYIGVAPNANNDVAPFEVRLYKN 120
    |||
QY 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILANPQFIS 177
    |||
DB 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILANPQFIS 177
    |||
```

```

RESULT 7
US-09-345-790-2
; Sequence 2, Application US/09345790
; Patent No. US20020099198A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,790
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/912,227
; FILING DATE:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-345-790-2
```

```

Query Match          95.3%; Score 906; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.1e-87;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 9 MPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFLQLETAKEPCMAKFGPLPSK 68
    |||
DB 1 MPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFLQLETAKEPCMAKFGPLPSK 60
    |||
QY 69 WQMASSPPCVNKSVDWKLELLQNGLYLYIGVAPNANNDVAPFEVRLYKNKDMIQTLT 128
    |||
DB 61 WQMASSPPCVNKSVDWKLELLQNGLYLYIGVAPNANNDVAPFEVRLYKNKDMIQTLT 120
    |||
QY 129 NKSQIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILANPQFIS 177
    |||
DB 121 NKSQIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILANPQFIS 169
    |||
```

RESULT 8

```
US-10-136-511-2
; Sequence 2, Application US/10136511
; Publication No. US20020168729A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
; FILE REFERENCE: 1488.0470007/EKS/PSC
; CURRENT FILING DATE: US/10/136,511
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/513,584
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/345,790
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/136,788
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/122,099
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 08/912,227
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: 60/024,058
; PRIOR FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-136-511-2
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Query Match 95.3%; Score 906; DB 13; Length 169;

Best Local Similarity 100.0%; Pred. No. 1.1e-87; Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 9 MFLSHRTOGAQRSSSKMLFCSIVMLFLCSFWLIFLQLEFAKPCMAKFGPLPSK 68
DB 1 MFLSHRTOGAQRSSSKMLFCSIVMLFLCSFWLIFLQLEFAKPCMAKFGPLPSK 60
QY 69 WOMASSEPPCVNKSVDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRLYNNKDMIQTLT 128
DB 61 WOMASSEPPCVNKSVDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRLYNNKDMIQTLT 120
QY 129 NKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNTYWGIIILLANQIFLS 177
DB 121 NKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNTYWGIIILLANQIFLS 169
```

RESULT 9

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US-10-338-083-17
; Sequence 17, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiya, Basil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-17
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Query Match 63.9%; Score 608; DB 14; Length 113;

Best Local Similarity 100.0%; Pred. No. 2.4e-56; Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 58 CMAKFGPLPSKQWASSSEPPCVNKSVDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 117
DB 1 CMAKFGPLPSKQWASSSEPPCVNKSVDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 60
QY 118 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNTYWGIIILL 170
DB 61 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNTYWGIIILL 113
```

RESULT 10

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US-10-611-399-17
; Sequence 17, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Dahiya, Basil I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT FILING DATE: US/10/611,399
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-399-17
```

Query Match 63.9%; Score 608; DB 16; Length 113;

Best Local Similarity 100.0%; Pred. No. 2.4e-56; Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 58 CMAKFGPLPSKQWASSSEPPCVNKSVDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 117
DB 1 CMAKFGPLPSKQWASSSEPPCVNKSVDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 60
QY 118 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNTYWGIIILL 170
DB 61 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNTYWGIIILL 113
```

RESULT 11

```
US-09-864-761-48455
; Sequence 48455, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
```

```

; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48455
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031599.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EST HUMAN HIT: BE270854.1, EVALU6 6.50e-01
; OTHER INFORMATION: SWISSPROT HIT: P25003, EVALU6 1.20e+00
US-09-864-761-48455
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Query Match          29.5%; Score 281; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 MCLSHENMPLSHSRTOGAORSSWKLMLFCSTIVMLFLCFSFSLFIPIOLE 52
Db 1 MCLSHENMPLSHSRTOGAORSSWKLMLFCSTIVMLFLCFSFSLFIPIOLE 52

RESULT 12
US-10-295-027-280
; Sequence 280, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natacha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glyme, Richard
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
```

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; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 280
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-280
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Query Match          9.0%; Score 85.5; DB 14; Length 377;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 32; Conservative 31; Mismatches 54; Indels 37; Gaps 6;
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Qy 26 LMLFCSIYV--LLFCFSFSLFIPIOLETAKEPCMAKGPUSKQWASSPPCNKUS 83
Db 127 IMFCKLVNPSAININPVLIIILLLELIMATVIA-----ARSSBDCKK-- 174
Qy 84 DWKLEILONGLYLIGVAPNANYNDVAPFEVRLYKNKMDIOTLNKSKIQVNGTYELH 143
Db 175 -----KGSMDSANIIDVDFPPARVLKSVSEVVIAGISAV--LGGITALN 218
Qy 144 VGDPTIDLFNSHQVLKXNTYWGIIILLANPOTIS 177
Db 219 VDDSV-----SGPHLSV---TFFWIIVACFPFAIA 245
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RESULT 13
US-10-424-599-201262
; Sequence 201262, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201262
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(246)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23765C.1.pcp
US-10-424-599-201262
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Query Match          8.4%; Score 79.5; DB 15; Length 246;
Best Local Similarity 22.9%; Pred. No. 6.1;
Matches 36; Conservative 21; Mismatches 55; Indels 45; Gaps 6;
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QY 22 SSMKMLPFSIMLMLELCSFMSLITIFILQLETAPECCAKGFLPSKMKMASSEPP----- 77
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Db 88 SKMKLEL-----AWLT--KALBPALQFC--WALPTANGKPPSPNNRS 128
      |||
QY 76 -----CVNKK--VSDMKLELLONGLYLYIGOVAVPNANVNDVAPFEVRLYKNDMLQTL 127
      |||
Db 123 LREITACTORSKTIQIOWMSLSDLTIGLYLYIRQASHPPEFDIDIGTQI----- 176
      |||
QY 128 TNRKSQNGVGYEALHVEDTIDILFNSEHOVLKNNTY 164
      |||
Db 177 LSESIVQDILYHIELAKGYRDNPPSLRNCMLRESY 213
      |||

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RESULT 14
US-10-149-310-52
: Sequence 52, Application US/10149310
: Publication No. US20040077039A1
: GENERAL INFORMATION:
: APPLICANT: Holtzman, Douglas
: APPLICANT: Madden, Kevin T.
: APPLICANT: Maxon, Mary
: APPLICANT: Sherman, Amir
: TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
: TITLE OF INVENTION: Zinc Binuclear Cluster Proteins
: FILE REFERENCE: 14184-019US1
: CURRENT APPLICATION NUMBER: US/10/149,310
: CURRENT FILING DATE: 2003-02-19
: PRIOR APPLICATION NUMBER: PCT/US01/29288
: PRIOR FILING DATE: 2001-09-19
: PRIOR APPLICATION NUMBER: US 60/233,564
: PRIOR FILING DATE: 2000-09-19
: NUMBER OF SEQ ID NOS: 308
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 52
: LENGTH: 879
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-10-149-310-52

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Query Match Similarity 8.4%; Score 79.5; Db 15; Length 879;
Best Local Similarity 22.7%; Pred No. 32;
Matches 37; Conservative 36; Mismatches 53; Indels 37; Gaps 8

QY 45 IFIFLQI--ETAKPCNAK-----FGPLPSKQWASSEPVCNKY----- 82
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Db 554 IFFIFKLLQDSIALDKVAKETIVLPSEDDNYKPLDTSNMTSSSEPRVDVQDGLFRE 613
                        : : : : :
QY 83 ----SDWK--LEIIIONGLYLYIGQVAPNAN-----NDVAPPEFVRLLYKKKMDQGLYTNRSK 132
                        : : : : :
Db 614 ALNEDDGKIHIEFVEPIITNVSADSTPSTPIPTNTA--TESYINKSDISNLVSKTD 670
                        : : : : :
QY 133 IQNVGATYELH-VGDTIDLIFNSEHOVLKNNTYWGITILLANDQ 174
                        : : : : :
Db 671 -ENIGTDSLVLGLPMSLILLFSDCVRIVRHNEYNYMLTYLPVPR 712
                        : : : : :

RESULT 15
US-10-149-310-50
; Sequence 50, Application US/10149310
; Publication No. US2004007039A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; APPLICANT: Madden, Kevin T.
; APPLICANT: Maxon, Mary
; APPLICANT: Sherman, Amir
; TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
; TITLE OF INVENTION: Zinc Binuclear Cluster Proteins
; FILE REFERENCE: 14184-013US1
; CURRENT APPLICATION NUMBER: US/10/149,310
; CURRENT FILING DATE: 2003-02-19
; PRIORITY APPLICATION NUMBER: PCT/US01/29288
; PRIORITY FILING DATE: 2001-09-19

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1 PRIOR APPLICATION NUMBER: US 60/233,564
2 PRIOR FILING DATE: 2000-09-19
3 NUMBER OF SEQ ID NOS: 308
4 SOFTWARE: PatentIn version 3.1
5 SEQ ID NO 50
6 LENGTH: 880
7 TYPE: CRT
8 ORGANISM: Saccharomyces cerevisiae
9 US-10-149-510-50

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	Query Match	8.1%;	Score 77.5;	DB 15;	Length 880;	
	Best Local Similarity	22.7%;	Pred. No. 52;			
	Matches	37;	Conservative	35;	Mismatches	54;
					Indels	37;
					Gaps	8;

QY	45	IPIFLQT-ETAKEPCMAK-----FGELPSKMOMASSEPPCVAKV-----	82
Db	555	IFSLTKLIODSTALDKRAKEIVILPSEDDNNXPLDTSNMTSSSEPRVDVQGLERE	614
QY	83	----SDMK--LEIIQNGUYLYIGVAAPKAN---YNDAPEFVRLLKKKDMMQLTINRSK	132
Db	615	ALNENDGKIHFVEKEPTTNVASDSTBESTPPIFTNLA--TESYYNKSDISKLVSKTD	671
QY	133	IQNVGGFTEHL-VGTTDLIPNSEHQVKKNNTYWGIIILLANDQ	174
Db	672	-ENIITGDLSLVLGNSSLILLETSCDCRIYRHAHEMYNYLTLPVLR	713

Search completed: November 2, 2004, 12:52:46
Job time : 130 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 12:27:21 ; Search time 39 Seconds
(without alignments)
300.982 Million cell updates/sec

Title: US-10-080-455-1

Perfect score: 951
Sequence: 1 MCISHENMPLSHRTQGAQ.....VLKNTYWGILLANPQFIS 177

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
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4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	906	95.3	169	2	US-08-912-227-2
2	906	95.3	169	4	US-09-513-584-2
3	906	95.3	169	4	US-09-345-790-2
4	84.5	8.9	1221	4	US-09-107-532A-3959
5	77.5	8.1	880	4	US-09-538-092-601
6	77	8.1	217	4	US-09-248-796A-20671
7	77	8.1	326	3	US-08-089-397A-11
8	77	8.1	326	6	5395759-2
9	77	8.1	2763	3	US-08-496-944-2
10	75.5	7.9	550	3	US-09-039-859-9
11	75	7.8	325	4	US-09-328-352-5760
12	74.5	7.8	271	4	US-09-443-041A-33
13	74.5	7.8	543	3	US-08-697-610-2
14	74.5	7.8	543	3	US-08-349-357-2
15	74	7.8	157	5	PCT-US93-02475-6
16	74	7.8	235	4	US-09-270-767-49088
17	74	7.8	567	4	US-09-645-926A-7
18	73.5	7.7	609	4	US-09-396-149-6
19	73	7.7	166	3	US-08-765-381-12
20	73	7.7	289	4	US-09-248-796A-15058
21	72.5	7.6	721	4	US-09-248-796A-18800
22	72	7.6	545	4	US-09-538-092-59
23	71.5	7.5	233	1	US-08-323-445A-10
24	71.5	7.5	233	1	US-08-515-903A-10
25	71.5	7.5	233	2	US-08-912-227-3
26	71.5	7.5	233	2	US-08-230-428B-2
27	71.5	7.5	233	3	US-08-883-086-6

28	71.5	7.5	233	3	US-08-880-342-37	Sequence 37, Appl
29	71.5	7.5	233	4	US-09-589-287B-3	Sequence 3, Appl
30	71.5	7.5	233	4	US-09-513-584-3	Sequence 3, Appl
31	71.5	7.5	233	4	US-09-157-864-9	Sequence 9, Appl
32	71.5	7.5	233	4	US-10-082-260-5	Sequence 5, Appl
33	71.5	7.5	233	4	US-09-345-790-3	Sequence 3, Appl
34	71.5	7.5	233	4	US-09-982-308B-22	Sequence 22, Appl
35	71.5	7.5	233	4	US-09-879-919-5	Sequence 5, Appl
36	71.5	7.5	233	4	US-09-588-947A-3	Sequence 3, Appl
37	71.5	7.5	233	4	US-09-131-237C-3	Sequence 3, Appl
38	71.5	7.5	233	4	US-09-589-286A-3	Sequence 3, Appl
39	71.5	7.5	233	4	US-09-005-874-3	Sequence 3, Appl
40	71.5	7.5	233	4	US-09-255-794A-3	Sequence 3, Appl
41	71.5	7.5	233	5	PCT-US93-12840-10	Sequence 10, Appl
42	71.5	7.5	233	6	5422425-2	Patent No. 5422425
43	71.5	7.5	633	3	US-08-860-048-11	Sequence 11, Appl
44	71.5	7.5	633	4	US-09-838-586-11	Sequence 11, Appl
45	71	7.5	157	5	PCT-US93-02475-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-912-227-2
; Sequence 2, Application US/08912227
; Patent No. 5998171
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endocrine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,227
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,058
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-227-2

Query Match 95.3%; Score 906; DB 2; Length 169;

Best local Similarity 100.0%; Pred. No. 2.8e-99;

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MPISHRTQAGRSSKMTWFCSTVWMLPFCSSWIFITFLQLETAKEPCMAKRGPIPSK 68

Db 1 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFLOLETAKPCAKFGPLPSK 60
QY 69 WQMASSEPPCVNKKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 128
Db 61 WQMASSEPPCVNKKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 120
QY 129 NKSQIÖNVGTYELHVGDTIDILINSEHQVKNNTYWGIIILANPOFIS 177
Db 121 NKSQIÖNVGTYELHVGDTIDILINSEHQVKNNTYWGIIILANPOFIS 169

RESULT 2

US-09-513-584-2
; Sequence 2, Application US/09513584
; Patent No. 6406867
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,
; ADDRESS: P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/513,584
; FILING DATE: 25-FEB-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,058
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,227
; FILING DATE: 15-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/122,099
; FILING DATE: 26-FEB-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/136,788
; FILING DATE: 28-MAY-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/345,790
; FILING DATE: 01-JUL-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-513-584-2

Query Match 95.3%; Score 906; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFLOLETAKPCAKFGPLPSK 68
Db 1 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFLOLETAKPCAKFGPLPSK 60
QY 69 WQMASSEPPCVNKKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 128
Db 61 WQMASSEPPCVNKKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 120
QY 129 NKSQIÖNVGTYELHVGDTIDILINSEHQVKNNTYWGIIILANPOFIS 177
Db 121 NKSQIÖNVGTYELHVGDTIDILINSEHQVKNNTYWGIIILANPOFIS 169

RESULT 3

US-09-345-790-2
; Sequence 2, Application US/09345790
; Patent No. 6521742
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,790
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,227
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-345-790-2

Query Match 95.3%; Score 906; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFLOLETAKPCAKFGPLPSK 68
Db 1 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFLOLETAKPCAKFGPLPSK 60
QY 69 WQMASSEPPCVNKKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 128
Db 61 WQMASSEPPCVNKKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 120
QY 129 NKSQIÖNVGTYELHVGDTIDILINSEHQVKNNTYWGIIILANPOFIS 177
Db 121 NKSQIÖNVGTYELHVGDTIDILINSEHQVKNNTYWGIIILANPOFIS 169

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RESULT 4
US-09-107-532A-3959
; Sequence 3959, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3959:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1221 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1221
; SEQUENCE DESCRIPTION: SEQ ID NO: 3959:
US-09-107-532A-3959

Query Match      8.9%; Score 84.5; DB 4; Length 1221;
Best Local Similarity 28.8%; Pred. No. 1.4;
Matches 19; Conservative 19; Mismatches 23; Indels 5; Gaps 1;

QY 102 APMANNDVAFPEVRLIKNDMTQTLNKS-----KIQNGYTELHVGDTIDLIENSEH 156
DB 515 APMGYQIDSSSEFSTIVAKNONTTTRTKKSTGSVELEKIGDLGGLPNNVFTYNSDN 574
QY 157 QVLKNN 162
DB 575 KVVKDN 580

RESULT 5
US-09-538-092-601
; Sequence 601, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gioc, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
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; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 601
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YML099C
US-09-538-092-601

Query Match      8.1%; Score 77.5; DB 4; Length 880;
Best Local Similarity 22.7%; Pred. No. 6;
Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;

QY 45 IFIFLOI---ETAKEPOMAK-----FGPLPSKQWASSPEPCVKNKY----- 82
DB 555 IFSEFLKIDSTALDKRAKEIIVLPSEDDNYKPLDTSNATSSSEPRVDVVOEGLFRE 614
QY 83 ----SPWK--LEIQNGKYLIIYQVAPNAN----YNDVAFPEVRLIKNDMTQTLNKS 132
DB 615 ALNENDGKHIEFEKPTNVSDSTSPSTPEIFTNIA---TESYNNKSDISKLVSKTD 671
QY 133 IQNVGTYELH-VGDTIDLIENSEHQLKNNYWGIIILANPQ 174
DB 672 -ENITGDSLIGLPNSIILIFSDCAIRVIRNEYNYLTLPVPR 713

RESULT 6
US-09-248-796A-20671
; Sequence 20671, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196,132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20671
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (15)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknc
US-09-248-796A-20671

Query Match      8.1%; Score 77; DB 4; Length 217;
Best Local Similarity 27.2%; Pred. No. 0.84; Indels 44; Gaps 7;
Matches 31; Conservative 13; Mismatches 13; Indels 26; Gaps 7;

QY 66 PSKQWASS--EPP-----CVNKVSDWKLEIIQNGLYLIIYQVAP---NANYNDVAPF 113
DB 85 PKQWMDAEKQWEPPLIVNPKCATGCGWEAPLIPNDHYI--GWPFPDINKPNVNGI--W 140
QY 114 EVRLIKNDMTQTLNKSQIYNGVT-YELHVGDTIDLIENSEHQLKNNYWG 166
DB 141 TPRLINPDIYYQVKTPEKLDKPIGIGFEL-----WSISDILFDNIYIG 185
```

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RESULT 7
US-08-089-397A-11
: Sequence 11, Application US/08089397A
: Patent No. 6086880
: GENERAL INFORMATION:
: APPLICANT: SABABA, MARTA I.J.
: APPLICANT: FRENCHICK, PATRICK J.
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: IJAZ, MOHAMMAD K.
: APPLICANT: GILCHRIST, JAMES E.
: APPLICANT: REDMOND, MARK J.
: TITLE OF INVENTION: ROTAVIRUS VACCINES
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/089,397A
: FILING DATE: 07-JUL-1993
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: ADLER, REID G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 29311-20003.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 326 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: US-08-089-397A-11

Query Match 8.1%; Score 77; DB 3; Length 326;
Best Local Similarity 22.8%; Pred. No. 1.6'
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9,

QY 26 LMFCSJYMLFLC-----SFSWLFIFLQLETKAPECMAR-----FGPLPSKQOM 71
Db 10 LTIISIIILNYYIKTITNTMDYIIFRLLILALISPFRTQNYGMYPITGSDAVYTN 69

QY 72 ASSEPP-----CV-----NKVSDWKLTELIONGLYIIGQVAPNA--NYNDVAPPEV 115
DbA 70 STSGEPFLTSLCLYPAKAKREISDDMENTLSQLFTKMPIGSVYFKYNDINTSV 129

QY 116 --RLYKNKDMIQTLTKNSKIONVGGTYELHVGDTIDLIENSEHOYLKNNTYGIIILANP 173
Db 130 NPQLYCDVNV-----LMRYNTSELDSASELADLIINE-----W-----LCNP 167

QY 174 QFIS 177
Db 168 MDIS 171

RESULT 8
US-08-089-397A-11
: Patent No. 5395759
: APPLICANT: HOLMES, IAN H.;DYALL-SMITH, MICHAEL L.
: TITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCE

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ENCODING THE HUMAN ROTAVIRUS MAJOR OUTER CAPSID GLYCOPROTEIN
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/474,642
FILING DATE: 29-APR-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 824,704
FILING DATE: 04-FEB-1987
SEQ ID NO: 2
LENGTH: 326
5395759-2

Query Match      8.1%; Score 77; DB 6; Length 326;
Best Local Similarity 22.8%; Pred. No. 1.6;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY      26 LMFQCSYVMLFLC-----SFSWLIFFILOETAKEPCMK-----FEPLESKQM 71
DB      10 LTLISLITLNYLTKTTTMDYITFLPLLIALISPVRTQNYGMPLITGSLDAVYN 69
QY      72 ASSEPP-----CV-----NKYSDWKLEILLONGLYAYGVADNA--NYNDVAPFEV 115
DB      70 STSEPEPLTSLCLYPAKAKNEISDDSEMENTLSGLFLTKGMPIGSVYFKQYNDINTSV 129
QY      116 --RIYKNDMTQTLTKSKIONVGTETLHVGDITDLFNSRHQVLKNNYTGIIILNP 173
DB      130 NPQLYCYNNVY-----LMRYDNTSLDASEIADLIINE-----W-----LCNP 167
QY      174 QFIS 177
DB      168 MDIS 171

RESULT 9
US-08-496-944-2
Sequence 2, Application US/08496944
Patent No. 6040496
GENERAL INFORMATION:
APPLICANT: Law, Marcus D
APPLICANT: Dietz, Jon M
TITLE OF INVENTION: Use of Translationally altered RNA to
TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
TITLE OF INVENTION: Monocotyledonous Plant Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,944
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1814
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-496-944-2

```

Best Local Similarity 25.0%; Pred. No. 38;
Matches 31; Conservative 20; Mismatches 53; Indels 20; Gaps 5;

QY 51 LEMAKPCMAKFGPLSKQMOMASSEPPCVNKMWDKLEILQNGLYLYGVANANVNDV 110

DB 18 IQPIKCRDNKFSHLPLWQVAFETIHYTDNOSKQMDV-SEALIKNTLTPPDANKASA 76

QY 111 APEV-RLYKNC-----DMIQTLTKSKIQNGVGYELHVPDIDLFENSEHQVLN-N 162

DB 77 ALLEVERMYNKRRESLKTDSLESFPRK-----ISPKSTINAAIMCDQOLKKNAN 125

QY 163 TYWG 166

DB 126 FVWG 129

RESULT 10

US-09-039-859-9

; Sequence 9, Application US/09039859

; Patent No. 6063987

; GENERAL INFORMATION:

; APPLICANT: Daub, Margaret E.

; APPLICANT: Ehrenshaft, Marilyn

; APPLICANT: Jenns, Ann E.

; TITLE OF INVENTION: Isolated Genes and Proteins Encoding

; TITLE OF INVENTION: Resistance to Photosensitizers

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESS: Virginia C. Bennett

; STREET: PO Box 37428

; CITY: Raleigh

; STATE: No. 6063987ch Carolina

; COUNTRY: US

; ZIP: 27627

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/039,859

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bennett, Virginia C.

; REGISTRATION NUMBER: 37,092

; REFERENCE/DOCKET NUMBER: 5405.333

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-854-1400

; TELEFAX: 919-854-1401

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 550 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-039-859-9

Query Match 7.9%; Score 75.5; DB 3; Length 550;

Best Local Similarity 18.5%; Pred. No. 5.1;

Matches 43; Conservative 33; Mismatches 55; Indels 101; Gaps 13;

QY 12 SHSRTQAGRSSWKLWFC--SIVMLFL--CSFSLFIPLQETAKPCMAKGPL 65

DB 188 SYSSVEG-----WRAHLGCHVLSVMAIFPKKSMTASWT---EQHEQAR--LMLQYSPL 236

QY 66 ---PSRK-----QMASSBP--PCVNKVSMDKLEI- 89

DB 237 NADSDRLAQYIRAEPLCEVSECVDLTNTSFYRDVADPATRNVPVQCCKIKLNMKGV 236

QY 90 --LQNGLYLYGVANANVNDVAFEVRLYKNCMDIQTLTKSKI----- 133

DB 297 QRLSRPLIMWEHVA-----TAYMHEPVLHTATNKDSFTAPYLAERLSITDF 343

QY 134 -----QNVGYTEL--HVGDIDLFENSEHQVLKNTYWGIIILANPOFI 176

DB 344 PPLVYQDHITAVYELTAAVQAVLDLFINYDK-----SLVASSISLV 385

RESULT 11

US-09-328-352-5760

; Sequence 5760, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 5760

; LENGTH: 325

; TYPE: PR

; ORGANISM: Acinetobacter baumannii

US-09-328-352-5760

Query Match 7.9%; Score 75; DB 4; Length 325;

Best Local Similarity 25.8%; Pred. No. 2.7;

Matches 42; Conservative 25; Mismatches 56; Indels 40; Gaps 8;

QY 31 SYMLFLCSFSLFIPLQETAKPCMAKFGPLSKQMOMASSEPPCVNKNY-----SDW 85

DB 80 SYLFLFGISLMPVYIILNI-----VNKY--LPSHERIRDLPFPKISITFTASIW 130

QY 86 KLEIILQNGLYLYGVYA--PNANYNDVAPREVELYKNCMDIQTLTKSKIQNGVGYELH 143

DB 131 FIYILRN-LILTYQVSLYGVCTVSWIAPFYAFYVNOQDIKFSKFK-----N 179

QY 144 VGDIDLFENSE-----QVLKNTYWGIIILANP 173

DB 180 IEDIIDIGASEHLKIFARDKLEKLETNKINSIHVAIFILVTP 222

RESULT 12

US-09-443-041A-33

; Sequence 33, Application US/09443041A

; Patent No. 6465717

; GENERAL INFORMATION:

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Orozco, Buddy

; APPLICANT: Rafalski, Antoni

; APPLICANT: Shen, Jennie

; TITLE OF INVENTION: Sterol Metabolism Enzymes

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/443,041A

; CURRENT FILING DATE: 1999-11-18

; PRIOR APPLICATION NUMBER: 60/109,283

; PRIOR FILING DATE: 1998-11-20

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 33

; LENGTH: 271

; TYPE: PR

; ORGANISM: Nicotiana tabacum

US-09-443-041A-33

Query Match 7.8%; Score 74.5; DB 4; Length 271;

Best Local Similarity 22.7%; Pred. No. 2.3;

Matches 34; Conservative 23; Mismatches 50; Indels 43; Gaps 9;

QY 10 PLSHSRTQAGRSSWKLWFC--SIVMLFLFIPLQETAKPCMAKGPL 48

DB 31 PLPH-MLQG-----WLRNYIGVLLYISGFLMCFYIHLKRVVYIPKDAIPSKAM 81

QY 49 -IQETAKPCMAKFGPLP--SKWQMASSBPCCVNKVS--WLEIILQNGLYLI---YQG 100

Db 82 ILQISVANK-AMPTVCALPSLSRVIEGNTKCFARISDVGLSVYTAALIVVERGI 140
QY 101 VAPNANVDAPFEVRLYKKNMDIQTITNK 130
Db 141 YMWHEMLDIKP-----LYKYIATHHTYNK 166

RESULT 13
US-08-697-610-2
; Sequence 2, Application US/08697610
; Patent No. 6172187
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: CD40 Associated Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,610
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,357
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-697-610-2

Query Match 7.8%; Score 74.5; DB 3; Length 543;

Best Local Similarity 25.5%; Pred. No. 6.6; Matches 36; Conservative 20; Mismatches 42; Indels 43; Gaps 8;

QY 30 CSIVMLFLCSEFSWILFLOLETAKEPCMAKFGPLPSKQWQMASSEPCVKNKVDW----- 85
Db 199 CVVWSCPHKCSVQTL-----LRSEGNQOIKX-----HEASSAVQHVMILKEMNSL 245
QY 86 --KLEILLONGLYLYGQVAPNAN-----YNDVAPFEVRLYKKNMDIQTITNKSQIONVGT 139
Db 246 EKQVSLIQLN-----ESYEKKKSIQSLHNQICSEFIEIRQKEMLR--NNESKI----- 291
QY 140 YELHVGDTIDLIENSEHQVLK 160
Db 292 --LHLQRYID-----SQAEKLR 306

RESULT 14
US-08-349-357-2
; Sequence 2, Application US/08349357
; Patent No. 6265556
; GENERAL INFORMATION:

; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: CD40 Associated Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,357
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-349-357-2

Query Match 7.8%; Score 74.5; DB 3; Length 543;

Best Local Similarity 25.5%; Pred. No. 6.6; Matches 36; Conservative 20; Mismatches 42; Indels 43; Gaps 8;

QY 30 CSIVMLFLCSEFSWILFLOLETAKEPCMAKFGPLPSKQWQMASSEPCVKNKVDW----- 85
Db 199 CVVWSCPHKCSVQTL-----LRSEGNQOIKX-----HEASSAVQHVMILKEMNSL 245
QY 86 --KLEILLONGLYLYGQVAPNAN-----YNDVAPFEVRLYKKNMDIQTITNKSQIONVGT 139
Db 246 EKQVSLIQLN-----ESYEKKKSIQSLHNQICSEFIEIRQKEMLR--NNESKI----- 291
QY 140 YELHVGDTIDLIENSEHQVLK 160
Db 292 --LHLQRYID-----SQAEKLR 306

RESULT 15

PCT-US93-02475-6
; Sequence 6, Application PC/TUS9302475
; GENERAL INFORMATION:
; APPLICANT: Winiateski, Bernadine J.
; TITLE OF INVENTION: Tumor Necrosis Factor with Modified
; TITLE OF INVENTION: Ion Channel
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Donald G. Lewis
; STREET: 8328 Regente Road #1B
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage
; COMPUTER: VE System 386
; OPERATING SYSTEM: MS-DOS 5
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/02475
FILING DATE: 19930412
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,625
FILING DATE: 12 March 1992
ATTORNEY/AGENT INFORMATION:
NAME: Donald G. Lewis
REGISTRATION NUMBER: 28636
REFERENCE/DOCKET NUMBER: BJW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2421
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Tumor Necrosis Factor (feline)
PUBLICATION INFORMATION:
AUTHORS: McGraw, R. A., Coffee, B.W., Otto,
AUTHORS: C.M., Drews, R.T. and Rawling, C.A.
TITLE: Gene Sequence of Feline Tumor Necrosis
TITLE: Factor '
JOURNAL: Nucleic Acids Research
VOLUME: 18
PAGES: 5564
DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO: 6: 1-157
PCT-US93-02475-6

Query Match 7.8%; Score 74; DB 5; Length 157;
Best Local Similarity 24.4%; Pred. No. 1.2;
Matches 30; Conservative 21; Mismatches 32; Indels 40; Gaps 6;

QY 81 KVSQDWKLEILQNGGLYLYIGQV-----APNANY---NDVAFPEVRLYKNKDWIQTLTNKS 131
Db 42 ELTDNQKLPSPSDGLYLSQVLTGQGCSPSTHVLTHAIRFAVSQTKVNLISAI--KS 99
QY 132 KION-----VGGTYELHVGDTID-----LIFNSEHQVLKKNITYWGI 167
Db 100 PCQRETPEGAEAKPWEPPIYLGWVFQLEKGRDRLSTEINLPAYLDPAESGQV-----YFGI 154
QY 168 ILL 170
Db 155 IAL 157

Search completed: November 2, 2004, 12:42:27
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 2, 2004, 11:53:00 / Search time 193 Seconds
(without alignments)
527.675 Million cell updates/sec

Title: US-10-080-455-1
Perfect score: 951
Sequence: 1 MCLSHLENNPLSHSRTOGAQ.....VLKNTYWGIIILLANPQFIS 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	177	1	TN18 HUMAN
2	951	100.0	177	2	AAH69111
3	951	100.0	177	2	AAH69319
4	418.5	44.0	173	2	Q80YG2
5	418.5	44.0	173	2	CAE12166
6	418.5	44.0	173	2	CAE12167
7	414.5	43.6	173	2	Q7TMY2
8	412.5	43.4	173	2	Q7TSS5
9	412.5	43.4	173	2	AAO55265
10	108.5	11.4	272	1	TNPS CHICK
11	88.5	9.3	273	2	Q74LW5
12	88.5	9.3	273	2	AAO80050
13	86.5	9.1	516	2	Q861B8
14	85.5	9.0	270	2	Q896D6
15	85.5	9.0	376	1	MLC1 HUMAN
16	85.5	9.0	377	2	Q6NSI6
17	85.5	9.0	377	2	AAH70042
18	85.5	9.0	377	2	CAG30346
19	85	8.9	3063	2	Q8QXN1
20	84	8.8	579	2	Q65C74
21	84	8.8	2074	2	Q6CST4
22	83.5	8.8	466	2	Q6CST4
23	83	8.7	599	2	Q81AM5
24	82	8.6	597	2	Q8GNC3
25	80.5	8.5	459	2	Q6HWM4
26	80	8.4	1181	2	Q96143
27	79.5	8.4	156	2	Q6D8W7
28	79.5	8.4	390	2	Q6LSR8
29	79.5	8.4	847	2	Q17701
30	79.5	8.4	847	2	Q6B1Y1
31	79.5	8.4	851	2	Q9LFL1

32	79	8.3	193	2	Q72VG7	Q72VG7 leptospira
33	79	8.3	193	2	Q8F914	Q8F914 leptospira
34	79	8.3	193	2	AA66957	AA66957 leptospira
35	79	8.3	326	2	Q805N8	Q805N8 human rotav
36	79	8.3	326	2	Q80AT3	Q80AT3 human rotav
37	79	8.3	372	1	PROB_OCEIH	Q8CUC5 oceanobacil
38	78.5	8.3	599	2	Q8E0H3	Q8E0H3 streptococc
39	78.5	8.3	599	2	Q8E648	Q8E648 streptococc
40	78.5	8.3	1061	2	Q7R934	Q7R934 plasmodium
41	78.5	8.3	1488	2	Q81DP7	Q81DP7 plasmodium
42	78	8.2	326	2	P89064	P89064 rotavirus
43	78	8.2	447	2	Q8GCK6	Q8GCK6 mycoplasma
44	78	8.2	564	1	Y61A MYCPN	P75041 mycoplasma
45	78	8.2	695	2	Q7R121	Q7R121 plasmodium

ALIGNMENTS

RESULT 1
TN18 HUMAN STANDARD; PRT; 177 AA.
ID TN18 HUMAN
AC Q9UNG2; Q95852; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 18 (Glucocorticoid-induced TNF-related ligand) (hgtrll) (Activation-inducible TNF-related ligand) (AIRL) (DNQ149/PRO175).
GN Name=TNFSF18; Synonyms=AIRL, GTRL, TL6;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RX MEDLINE=99175482; PubMed=10074428;
RA Gurney A.L., Masters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GTR.";
RT Curr. Biol. 9:215-218(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Hang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshigiri S., Simmons L., Singh U., Smith V., Stinson J., Vagstad A., Vanden R., Watanabe C., Wleand D., Woods K., Xie W.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RT Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE OF 9-177 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156876; PubMed=10037686;
RA Kwon B., Yu K.-Y., Ni U., Yu G.-L., Jang I.-K., Kim Y.-U., Xing L., Liu D., Wang S.-X., Kwon B.S.;
RT "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";
RT J. Biol. Chem. 274:6056-6061(1999).
CC -!- FUNCTION: Cytokine that binds to TNFSF18/AIRL/GTR. Important for interactions between activated T lymphocytes and endothelial cells and may modulate T lymphocyte survival in peripheral tissues.
CC -!- SUBUNIT: Homotrimer (Potential).

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CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Expressed at high levels in the small
CC intestine, ovary, testis, kidney and endothelial cells.
CC -1- INDUCTION: Up-regulated after stimulation by lipopolysaccharides.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF15303; AAD22634.1; -.
DR EMBL; AY358868; AAQ89227.1; -.
DR EMBL; AF117713; AAD19695.1; -.
DR Genew; HGNC:11932; TNFSF18.
DR MIM; 603898; -.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_1-like.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; FALSE_NEG.
DR CycloLine; Glycoprotein; Signal-anchor; Transmembrane.
KW CycloLine; Glycoprotein; Signal-anchor (Potential).
FT TRANSMEM 1 28 Cytosolic (Potential).
FT TRANSMEM 29 49 Signal-anchor for type II membrane
FT TRANSMEM 50 177 protein (Potential).
FT CARBOHYD 129 129 Extracellular (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;

Query Match 100.0%; Score 951; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPISHRTQGAQRSSWKLWLFCSIVWLFLFCSPSWLFIPLQLETAKEPCMA 60
DB 1 MCLSHLEMPISHRTQGAQRSSWKLWLFCSIVWLFLFCSPSWLFIPLQLETAKEPCMA 60
QY 61 KFGPLPSKQWASSPEPCVNVKVSQDKLEILQNGLYLYIGQVAPNANVNDVAPFEVRLTKN 120
DB 61 KFGPLPSKQWASSPEPCVNVKVSQDKLEILQNGLYLYIGQVAPNANVNDVAPFEVRLTKN 120
QY 121 KDMQTLTNKSKIQNVGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILANPOFIS 177
DB 121 KDMQTLTNKSKIQNVGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILANPOFIS 177

RESULT 2
AAH69111 PRELIMINARY; PRT; 177 AA.
AC AAH69111;
DT 24-MAY-2004 (TREMBlrel. 27, Created)
DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein (Fragment).
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Synthetic constructs;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Roak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gamaratte P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Synthetic constructs;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069111; AAH69111.1; -.
FT NON TER 1 1
SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;

Query Match 100.0%; Score 951; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPISHRTQGAQRSSWKLWLFCSIVWLFLFCSPSWLFIPLQLETAKEPCMA 60
DB 1 MCLSHLEMPISHRTQGAQRSSWKLWLFCSIVWLFLFCSPSWLFIPLQLETAKEPCMA 60
QY 61 KFGPLPSKQWASSPEPCVNVKVSQDKLEILQNGLYLYIGQVAPNANVNDVAPFEVRLTKN 120
DB 61 KFGPLPSKQWASSPEPCVNVKVSQDKLEILQNGLYLYIGQVAPNANVNDVAPFEVRLTKN 120
QY 121 KDMQTLTNKSKIQNVGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILANPOFIS 177
DB 121 KDMQTLTNKSKIQNVGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILANPOFIS 177

RESULT 3
AAH69319 PRELIMINARY; PRT; 177 AA.
AC AAH69319;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein.
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Roak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gamaratte P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Synthetic constructs;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069111; AAH69111.1; -.
FT NON TER 1 1
SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyanski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC069319; AA069319.1; -;
 SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;

Query Match 100.0%; Score 951; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 1.2e-80;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKMLFCSTVWTLFLCSPSWLIFFLQLETKAPECPMA 60
 DB 1 MCLSHLENMPLSHSRTOGAQRSSWKMLFCSTVWTLFLCSPSWLIFFLQLETKAPECPMA 60
 QY 61 KFGPLPSKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAPNANYNDVAPFEVRLYKN 120
 DB 61 KFGPLPSKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAPNANYNDVAPFEVRLYKN 120
 QY 121 KDMIQTLTKSKIQNVGTYELHVGDTIDLINSEHOVLKNNYWGIIILANPQFIS 177
 DB 121 KDMIQTLTKSKIQNVGTYELHVGDTIDLINSEHOVLKNNYWGIIILANPQFIS 177

RESULT 4
 Q80YG2 PRELIMINARY; PRT; 173 AA.

AC Q80YG2;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
 DE GTR ligand.
 GN Name="tnfsf18; Synonyms=tnfsf 18;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2J;
 RA Bianchini R., Nocentini G., Ronchetti S., Ayroldi E., Riccardi C.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/Ca;
 RX PubMed=14608036;
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,
 RA Waldmann H.;
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is
 RT costimulatory for T cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).
 DR EMBL: AY342223; AAC09011.1; -;
 DR EMBL: AJ577579; CAE12166.1; -;
 DR EMBL: AJ577580; CAE12167.1; -;
 DR MGD: MGI:2673064; Tnfef18.
 DR GO: GO:0016020; C:membrane, IEA.
 DR GO: GO:0005164; P:tumor necrosis factor receptor binding, IEA.
 DR InterPro: IPR008983; TNF like.
 DR InterPro: IPR003636; TNF subf.
 DR ProDom: PD002012; TNF subf. 1.
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 44.0%; Score 418.5; DB 2; Length 173;
 Best Local Similarity 52.6%; Pred. No. 5.6e-31;

Matches 92; Conservative 20; Mismatches 58; Indels 5; Gaps 5;
 QY 6 LENMPLSHSRTOGAQRSSWKMLFCSTVWTLFLCSPSWLIFFLQLETKAPECPMAKFGP 64
 DB 1 MEMPRESPPQRAERCK-KSWLICTVALMLLCSLGTLYSLK-PTAIESCMVAFEL 58
 QY 65 LPKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAP-NANY-NDVAPFEVRLYKNKD 122
 DB 59 SSSKWMHTSPKPCVNTTSGKRLTIQSGTYLYIGQVTPYDKKYLKONAFVVGQIYKND 118
 QY 123 MIQTLTKSKIQNVGTYELHVGDTIDLINSEHOVLKNNYWGIIILANPQFIS 177
 DB 119 VLQTLNMDPQILPIGTYELHAGDNILYLFKNSKDIQKNNYWGIIILMDLPFIS 173

RESULT 5
 CAE12166 PRELIMINARY; PRT; 173 AA.

AC CAE12166;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE GTR ligand.
 GN TNFSF 18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/Ca;
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,
 RA Waldmann H.;
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is
 RT costimulatory for T cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).
 DR EMBL: AJ577579; CAE12166.1; -;
 KM Alternative splicing.
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 44.0%; Score 418.5; DB 2; Length 173;
 Best Local Similarity 52.6%; Pred. No. 5.6e-31;
 Matches 92; Conservative 20; Mismatches 58; Indels 5; Gaps 5;

QY 6 LENMPLSHSRTOGAQRSSWKMLFCSTVWTLFLCSPSWLIFFLQLETKAPECPMAKFGP 64
 DB 1 MEMPRESPPQRAERCK-KSWLICTVALMLLCSLGTLYSLK-PTAIESCMVAFEL 58
 QY 65 LPKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAP-NANY-NDVAPFEVRLYKNKD 122
 DB 59 SSSKWMHTSPKPCVNTTSGKRLTIQSGTYLYIGQVTPYDKKYLKONAFVVGQIYKND 118
 QY 123 MIQTLTKSKIQNVGTYELHVGDTIDLINSEHOVLKNNYWGIIILANPQFIS 177
 DB 119 VLQTLNMDPQILPIGTYELHAGDNILYLFKNSKDIQKNNYWGIIILMDLPFIS 173

RESULT 6

CAE12167 PRELIMINARY; PRT; 173 AA.
 AC CAE12167;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE GTR ligand.
 GN TNFSF 18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/Ca;

RA Tone M., Tone Y., Adams B., Yates S.F., Frewin M.R., Cobbold S.P.,
 RA Waldmann H.;
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is
 RT costimulatory for T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).
 DR EMBL; AJ577580; CAB2167.1; -.
 KM Alternative splicing.
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 44.0%; Score 418.5; DB 2; Length 173;
 Best Local Similarity 52.0%; Pred. No. 5,6e-31;
 Matches 92; Conservative 20; Mismatches 58; Indels 5; Gaps 5;

QY 6 LENMPLSHSRTOGAQRSSWKMLFCSIVMLL-FLCSFSLIFLQLETAKEPCAKRGP 64
 Db 1 MEEMPLRSPQRAERCK-KSWLCTIVALLMLLCSLGLTYTSIK-PTVIESCWVKFEL 58
 QY 65 LPSKQWASSEPPCNKVSMDKLETLONGLYLYGVAP-NANY-NDVAFPEVRLYKXND 122
 Db 59 SSSKWHMTSPKPHCVNTTSDGKTLQSGTYLYIQVAVPVDKXIKDNAPFVQYKXND 118
 QY 123 MIQTLNKSQKIQNVGTYELHVGDTIDLFENSEHVLKNNYWGIIILANPOFIS 177
 Db 119 VIQTLNMDFQLPLPGVYELHAGDNITYLKFNKSKHIQKNTYWGIIIMDLPFIS 173

RESULT 7

QY 7 Q7TNY2 PRELIMINARY; PRT; 173 AA.

ID Q7TNY2
 AC Q7TNY2;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE GTR ligand.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=14647196;
 RA Kim J.D., Choi B.K., Bae J.S., Lee U.H., Han I.S., Lee H.W.,
 RA Youn B.S., Vinay D.S., Kwon B.S.;
 RT "Cloning and characterization of GTR ligand";
 RL Genes Immun. 4:564-569(2003).
 DR EMBL; AY267900; AAP96745.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR003636; TNF subf.
 DR Prodom; PD002012; TNF subf. 1.
 SQ SEQUENCE 173 AA; 19773 MW; 1FD22953BCFC34C5 CRC64;

Query Match 43.6%; Score 414.5; DB 2; Length 173;
 Best Local Similarity 52.0%; Pred. No. 1,3e-30;
 Matches 91; Conservative 20; Mismatches 59; Indels 5; Gaps 5;

QY 6 LENMPLSHSRTOGAQRSSWKMLFCSIVMLL-FLCSFSLIFLQLETAKEPCAKRGP 64
 Db 1 MEEMPLRSPQRAERCK-KSWLCTIVALLMLLCSLGLTYTSIK-PTVIESCWVKFEL 58
 QY 65 LPSKQWASSEPPCNKVSMDKLETLONGLYLYGVAP-NANY-NDVAFPEVRLYKXND 122
 Db 59 SSSKWHMTSPKPHCVNTTSDGKTLQSGTYLYIQVAVPVDKXIKDNAPFVQYKXND 118
 QY 123 MIQTLNKSQKIQNVGTYELHVGDTIDLFENSEHVLKNNYWGIIILANPOFIS 177
 Db 119 VIQTLNMDFQLPLPGVYELHAGDNITYLKFNKSKHIQKNTYWGIIIMDLPFIS 173

RESULT 8

Q7TS55

ID Q7TS55 PRELIMINARY; PRT; 173 AA.

AC Q7TS55;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE GTR ligand (glucocorticoid-induced-tumor necrosis factor receptor
 DE ligand).
 GN Name=Gitr1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57/Bl6; TISSUE=spleen;
 RA Ji H., Tenhout C.;
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/J;
 RX MEDLINE=22883945; PubMed=14521928;
 RA Yu K.Y., Kim H.S., Song S.Y., Min S.S., Jeong J.U., Youn B.S.;
 RT "Identification of a ligand for glucocorticoid-induced tumor necrosis
 RT factor receptor constitutively expressed in dendritic cells.";
 RL Biochem. Biophys. Res. Commun. 310:433-438(2003).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/J;
 RA Yu K.-Y., Min S.S., Youn B.-S.;
 RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY320040; AAP70494.1; -.
 DR EMBL; AY359852; AA055265.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR003636; TNF subf.
 DR Prodom; PD002012; TNF subf. 1.
 KM Receptor.
 SQ SEQUENCE 173 AA; 19732 MW; 0F08494CACF424D2 CRC64;

Query Match 43.4%; Score 412.5; DB 2; Length 173;
 Best Local Similarity 52.0%; Pred. No. 2e-30;
 Matches 91; Conservative 20; Mismatches 59; Indels 5; Gaps 5;

QY 6 LENMPLSHSRTOGAQRSSWKMLFCSIVMLL-FLCSFSLIFLQLETAKEPCAKRGP 64
 Db 1 MEEMPLRSPQRAERCK-KSWLCTIVALLMLLCSLGLTYTSIK-PTVIESCWVKFEL 58
 QY 65 LPSKQWASSEPPCNKVSMDKLETLONGLYLYGVAP-NANY-NDVAFPEVRLYKXND 122
 Db 59 SSSKWHMTSPKPHCVNTTSDGKTLQSGTYLYIQVAVPVDKXIKDNAPFVQYKXND 118
 QY 123 MIQTLNKSQKIQNVGTYELHVGDTIDLFENSEHVLKNNYWGIIILANPOFIS 177
 Db 119 VIQTLNMDFQLPLPGVYELHAGDNITYLKFNKSKHIQKNTYWGIIIMDLPFIS 173

RESULT 9

AA055265 PRELIMINARY; PRT; 173 AA.

ID AA055265
 AC AA055265;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Glucocorticoid-induced-tumor necrosis factor receptor ligand.
 GN GTR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

ID	TNFS	CHICK	STANDARD	PRT	272	AA
AC	Q91BD8					
DT	28-FEB-2003	(Rel. 41, Created)				
DT	29-MAR-2004	(Rel. 43, Last sequence update)				
DT	05-JUL-2004	(Rel. 44, Last annotation update)				
DE	Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).					
GN	Name=TNFSF5; Synonyms=CD40LG, CD40L,					
OS	Gallus gallus (Chicken).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Archosauiria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;					
OC	Gallus.					
OX	NCBI_TaxID=9031;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=White leghorn; TISSUE=Spleen;					
RC	Tregaskes C.A., Young J.R., Burnside J.;					
RT	"Cloning of a putative chicken CD40 ligand. "					
RT	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.					
CC	-1- FUNCTION: Cyclokin that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).					
CC	-1- SUBUNIT: Homotrimer (By similarity).					
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).					
CC	-1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).					
CC	-1- SIMILARITY: Belongs to the tumor necrosis factor family.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
OR	EMBL; AJ243435; CAB95748.2; -					

DR EMBL; AE017200; AAS08050.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 273 AA; 31108 MW; 34414AF96D1747A8 CRC64;
Query Match 9.3%; Score 88.5; DB 2; Length 273;
Best local Similarity 23.6%; Pred. No. 5.9;
Matches 42; Conservative 32; Mismatches 47; Indels 57; Gaps 10;
QY 27 WLFPSVLMFLGSPSWLIFLQLETAKEPCMAKFGPLPSKQW---ASSEPPCVNKVS 83
DB 8 WIF---LIVFVG---INIFLGIELMQPTLLSAGSTPQDTIKSETSDQITIPKVN 58
QY 84 DMKLEILLONGYLT-----IYGVAFNANYNVA-----PEFVRLYKXKDM 123
DB 59 DKQ---EDGYTLAKKNDSDWIKATQGVKQVNNSENLSVHLDPITLSKXKKEAL 114
QY 124 IQLTLNKSQIONV--GGTY---ELHVGDTIDLIENSE-----HOVLKKN 162
DB 115 REVWRPFKDSQNVYQGNKYTYLSLSESD--DYIFNQTKYGEFFAATARLHIIVKN 170
RESULT 12
AAS08050 PRELIMINARY; PRT; 273 AA.
AC AAS08050;
DT 02-MAR-2004 (TREMblrel. 27, Created)
DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein.
GN IJ0068.
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC 533;
RX PubMed=14966310;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
Pitcec A.-C., Zwielen M.-C., Rouvet M., Altermann E., Barragou R.,
Mollet B., Mercetier A., Kleenhammer T., Arigoni F., Scheil M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
Lactobacillus johnsonii NC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
DR EMBL; AE017200; AAS08050.1; -
KW Hypothetical protein.
SQ SEQUENCE 273 AA; 31108 MW; 34414AF96D1747A8 CRC64;
Query Match 9.3%; Score 88.5; DB 2; Length 273;
Best local Similarity 23.6%; Pred. No. 5.9;
Matches 42; Conservative 32; Mismatches 47; Indels 57; Gaps 10;
QY 27 WLFPSVLMFLGSPSWLIFLQLETAKEPCMAKFGPLPSKQW---ASSEPPCVNKVS 83
DB 8 WIF---LIVFVG---INIFLGIELMQPTLLSAGSTPQDTIKSETSDQITIPKVN 58
QY 84 DMKLEILLONGYLT-----IYGVAFNANYNVA-----PEFVRLYKXKDM 123
DB 59 DKQ---EDGYTLAKKNDSDWIKATQGVKQVNNSENLSVHLDPITLSKXKKEAL 114
QY 124 IQLTLNKSQIONV--GGTY---ELHVGDTIDLIENSE-----HOVLKKN 162
DB 115 REVWRPFKDSQNVYQGNKYTYLSLSESD--DYIFNQTKYGEFFAATARLHIIVKN 170
RESULT 13
Q861B8 PRELIMINARY; PRT; 516 AA.
AC Q861B8;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Hypothetical protein.

OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Richinger L., Szafranski K., Pachepat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116511; AAO52204.1; -
KW Hypothetical protein.
SQ SEQUENCE 516 AA; 58667 MW; 80B308CF6CDF97C2 CRC64;
Query Match 9.1%; Score 86.5; DB 2; Length 516;
Best local Similarity 29.0%; Pred. No. 19;
Matches 27; Conservative 17; Mismatches 36; Indels 13; Gaps 3;
QY 80 NKVSDMKLEILLONGYLYIGVAPNANYNVAPFEVRLYKXKDMIQTLNKSQIONVGGT 139
DB 419 NETPDSKLT-----IYIY-----NIEKDPVQPTVIEFKDEINEMITKHFQIENNDS 469
QY 140 YELHVGDTIDLIENSEHQVLKNNYWGIIILAN 172
DB 470 VNNINENKDPFLIN---IPKDGNCDSGIILLTN 498
RESULT 14
Q896D6 PRELIMINARY; PRT; 270 AA.
AC Q896D6;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE K11A protein, putative phage-related DNA binding protein.
GN Name=K11A; OrderedLocustNames=CTC01071;
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / E88;
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baewer S., Fricke W.F., Wietzer A., Liesegang H.,
Ra Deckert I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Goetschalck G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321 (2003).
DR EMBL; AE015939; AAO35654.1; -
DR InterPro; IPR003497; BRO_N.
DR Pfam; PF02498; Bro-N; 1.
KW Complete proteome.
SQ SEQUENCE 270 AA; 31533 MW; C378AB524C0133A8 CRC64;
Query Match 9.0%; Score 85.5; DB 2; Length 270;
Best local Similarity 25.4%; Pred. No. 11;
Matches 31; Conservative 18; Mismatches 36; Indels 37; Gaps 5;
QY 81 KVSDMKLEILLONGYLYIGVAPNANYNVAPFEVRLYKXKDMIQTLNKSQIONVGGT 139
DB 134 KAKKMKLEILLONGYLYIGVAPNANYNVAPFEVRLYKXKDMIQTLNKSQIONVGGT 186
QY 140 -----YELHVG-----DTIDLIENSEHQVLKNNYWGIIIL 170

- DB 187 LINKLHLEKVOYKQNDQWLLYKHSKGXTHSETIDIVRSDDGPRDPVMMTKTQGRLL 246
- QY 171 AN 172
- DB 247 YN 248
- RESULT 15
- ID MLC1 HUMAN STANDARD: PRT; 376 AA.
- AC 015049: O8TAGS: G9UG8;
- DT 15-JUL-1998 (Rel. 36, Created)
- DT 05-JUL-2004 (Rel. 44, Last sequence update)
- DT 05-JUL-2004 (Rel. 44, Last annotation update)
- DE Membrane protein MLC1.
- GN Name=MLC1; Synonyms=WKL1, KIAA0027;
- OS Homo sapiens (Human)
- OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
- OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
- OX NCBI_TaxID=9606;
- LN [1]
- RP SEQUENCE FROM N.A.
- RC TISSUE=Bone marrow;
- RX MEDLINE=96051387; PubMed=7584026;
- RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
- RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
- RT "Prediction of the coding sequences of unidentified human genes. I.
- RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
- RT analysis of randomly sampled cDNA clones from human immature myeloid
- RT cell line KG-1.";
- RL DNA Res. 1:27-35(1994).
- LN [2]
- RP REVISIONS.
- RX MEDLINE=22158633; PubMed=12168954;
- RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
- RT "Construction of expression-ready cDNA clones for KIAA genes: manual
- RT curation of 330 KIAA cDNA clones.";
- RL DNA Res. 9:99-106(2002).
- LN [3]
- RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANT PC MET-308.
- RC TISSUE=Hippocampus;
- RX MEDLINE=21252990; PubMed=11326298; DOI=10.1038/sj/mp.4000869;
- RA Meyer U., Huberth A., Ortega G., Sygallio Y.V., Jatzke S.,
- RA Moesner R., Strom T.M., Ulzheimer-Teuber I., Sceder G., Schmitt A.,
- RA Lesch K.P.;
- RT "A missense mutation in a novel gene encoding a putative cation
- RT channel is associated with catatonic schizophrenia in a large
- RT pedigree.";
- RL Mol. Psychiatry 6:302-306(2001).
- LN [4]
- RP SEQUENCE FROM N.A.
- RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
- RA Dunham I., Hunt A.R., Collins J.E., Buskiewich R., Beare D.M.,
- RA Clamp M., Smith L.J., Ainscough R., Almeida J.P., Babage A.K.,
- RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
- RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
- RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
- RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
- RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
- RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
- RA Evans K.L., Fey U.M., Fleming K., French L., Garner A.A.,
- RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
- RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
- RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
- RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
- RA Marzyn I.D., Mashneghi-Mohammadi M., Matthews L.H., Mccann O.T.,
- RA Mcgill J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
- RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
- RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Rose M.T.,
- RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
- RA Soderlund C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M.,
- RA Vaudin M., Wallis J., Wallis J.M., Whiteley M.N., Willey D.L.,
- RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
- RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
- RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
- RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
- RA Roe B.A., Chen F., Chu L., Crabtree J., Aoki N., Mitsuyama S.,
- RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
- RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
- RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
- RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
- RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mink P.,
- RA Fullon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
- RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
- RA Hinds K., Kemp K., Lettreille P., Layman D., Ozersky P., Rohlfing T.,
- RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
- RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
- RA Wilson R., Emanuel B.S., Shaikh T., Kurashiki H., Saita S.,
- RA Budart M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
- RA Edelman L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
- RA Peyriard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
- RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
- RA Khan A.S., Lane L., Tlathun Y., Wright H.;
- RT "The DNA sequence of human chromosome 22.";
- RL Nature 402:489-495(1999).
- LN [5]
- RP SEQUENCE FROM N.A.
- RC TISSUE=Brain;
- RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
- RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
- RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
- RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
- RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
- RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
- RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
- RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
- RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
- RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
- RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
- RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
- RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
- RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
- RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
- RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
- RA Buterfield Y.S.N., Krzywdinski M.I., Skalska U., Smailus D.E.,
- RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
- RT "Generation and initial analysis of more than 15,000 full-length human
- RT and mouse cDNA sequences.";
- RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
- LN [6]
- RP SEQUENCE OF 1-13.
- RC TISSUE=Platelet;
- RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt010;
- RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
- RA Thomas G.R., Vandekerckhove J.;
- RT "Exploring proteomes and analyzing protein processing by mass
- RT spectrometric identification of sorted N-terminal peptides.";
- RL Nat. Biotechnol. 21:566-569(2003).
- LN [7]
- RP VARIANTS MLC ILEU-92; ARG-211 AND LEU-279.
- RX MEDLINE=21152271; PubMed=11254442;
- RA Leegwater P.A.J., Yuan B.Q., van der Steen J., Mulders J.,
- RA Koenst A.A.M., Ijla Boor P.K., Mejaski-Bosnjak V.,
- RA van der Maarel S.M., Frants R.R., Oudejans C.B.M., Schutgens R.B.H.,
- RA Pronk J.C., van der Knapp M.S.;
- RT "Mutations of MLC1 (KIAA0027), encoding a putative membrane protein,
- RT cause megalencephalic leukoencephalopathy with subcortical cysts.";
- RL Am. J. Hum. Genet. 68:831-838(2001).
- LN [8]
- RP VARIANTS MLC SER-91; IYS-140 AND SER-140.
- RX PubMed=11935341; DOI=10.1007/s00439-002-0682-x;
- RA Leegwater P.A.J., Boor P.K.I., Yuan B.Q., van der Steen J., Visser A.,
- RA Kont A.M., Oudejans C.B.M., Schutgens R.B.H., Pronk J.C.,
- RA van der Knapp M.S.;
- RT "Identification of novel mutations in MLC1 responsible for
- RT megalencephalic leukoencephalopathy with subcortical cysts.";

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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:41:46 ; Search time 155 Seconds
(without alignments)
291.612 Million cell updates/sec

Title: US-10-080-455-1_COPY_52_177

Sequence: 1 ETAKEDCMAKFGPLPSKWM.....VLKNTYWGILILANQFIS 126

Scoring table: BLOSUM62

Gapor 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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1: Genesegp.23sep04.*
  A: Genesegp.1980s.*
  1: Genesegp.1990s.*
  2: Genesegp.2000s.*
  3: Genesegp.2001s.*
  4: Genesegp.2002s.*
  5: Genesegp.2003s.*
  6: Genesegp.2003bs.*
  7: Genesegp.2003bs.*
  8: Genesegp.2004s.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	IDB	ID	Description
1	675	100.0	169	2	AAW37847	Aaw37847 Human ent
2	675	100.0	169	3	AAB08785	Rab08785 A human e
3	675	100.0	169	3	AA553061	Ray553061 Human ent
4	675	100.0	169	6	ADAI1464	Adai1464 Human ent
5	675	100.0	169	7	ADCO1858	Adco1858 Human Ent
6	675	100.0	177	2	AAI15817	Ray15817 Human act
7	675	100.0	177	2	AAV06646	Ray06646 Human PR
8	675	100.0	177	4	AAB47056	Rab47056 PRO175. 5
9	675	100.0	177	4	AAB20109	Rab20109 Human imm
10	675	100.0	177	4	AAB53065	Rab53065 Human act
11	675	100.0	177	4	AAB47287	Rab47287 PRO175 po
12	675	100.0	177	5	AA850979	Rab50979 Human PR
13	675	100.0	177	5	AAU81953	Rau81953 Human PR
14	675	100.0	177	6	ABR43233	Abri43233 Human GI
15	675	100.0	177	6	ABP60544	Abp60544 Human tun
16	675	100.0	177	7	ADC35222	Adc35222 Human TNH
17	675	100.0	177	7	ABM02285	Abm02285 Human ent
18	566	83.9	508	4	ABG17426	Abg17426 Novel hun
19	84.5	12.5	1221	7	ADP29332	Adp29332 E. faecit
20	78.5	11.6	599	9	ABP25933	Abp25933 Streptococ
21	77	11.4	183	3	AAG43532	Rag43532 Arabidops
22	77	11.4	228	3	AAG43533	Rag43533 Arabidops
23	77	11.4	230	3	AAG43531	Rag43531 Arabidops
24	77	11.4	851	5	ABB93512	Abb93512 Herbicide
25	76	11.3	2763	2	AAW10344	Maize dwm

ALIGNMENTS

26	75	11.2	5795	4	AAU37017	Aau37017	Staphyloc						
27	75	11.1	332	8	ADK16905	Adk16905	Nanorachna						
28	74	11.0	157	2	AAK41859	Aak41859	Feline TN						
29	74	11.0	472	2	AAK98835	Aak98835	CD40 asso						
30	74	11.0	516	2	AAW27436	Aaw27436	Human CRA						
31	74	11.0	543	2	AAK98833	Aak98833	CD40 asso						
32	74	11.0	543	2	AAW27432	Aaw27432	Human CRA						
33	74	11.0	543	6	ABO07169	Ab007169	Human p53						
34	74	11.0	567	2	AAK99259	Aak99259	Full-length						
35	74	11.0	567	4	AAK67615	Aak67615	Amino aci						
36	74	11.0	567	5	AAO17756	Aao17756	Murine CD						
37	74	11.0	567	5	ABBS7054	Abbs7054	Mouse jcs						
38	74	11.0	567	7	ADD25542	Add25542	Binding d						
39	74	11.0	568	2	AAW03146	Aaw03146	IMPI asse						
40	74	11.0	568	2	AAW27431	Aaw27431	Human CRA						
41	74	11.0	568	3	AAK98166	Aak98166	Human TRP						
42	74	11.0	568	5	AAO17757	Aao17757	Human CD4						
43	74	11.0	568	6	ABO07171	Ab007171	Human p53						
44	74	11.0	568	7	ADB80964	Adb80964	RING-SH C						
45	74	11.0	568	7	ADB80957	Adb80957	RING-SH C						
ALIGNMENTS													
RESULT 1													
AAW37847													
ID	AAW37847	standard;	protein;	169	AA.								
XX	AAW37847;												
AC													
XX													
DT	28-AUG-1998	(first	entry)										
XX													
DE	Human endokine-alpha.												
XX													
KM	Endokine-alpha; cytokine; tumour necrosis factor; human;												
KM	immunomodulation; infection; cell proliferation; angiogenesis; tumour;												
KW	metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;												
KW	diagnosis; therapy.												
XX													
OS	Homo sapiens.												
XX													
PH	Key	Location/Qualifiers											
FT	Domain	1..17											
FT	Domain	/note="intracellular domain"											
FT	Domain	18..43											
FT	Domain	/note="transmembrane domain"											
FT	Domain	44..169											
FT	Peptide	/note="extracellular domain"											
FT	Peptide	44..158											
FT	Peptide	/note="epitope-bearing fragment (Claim 13)"											
FT	Peptide	44..54											
FT	Peptide	/note="epitope-bearing fragment (Claim 13)"											
FT	Peptide	57..68											
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FT	Peptide	69..78											
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FT	Peptide	94..105											
FT	Peptide	/note="epitope-bearing fragment (Claim 13)"											
FT	Peptide	108..132											
FT	Peptide	/note="epitope-bearing fragment (Claim 13)"											
FT	Peptide	142..158											
FT	Peptide	/note="epitope-bearing fragment (Claim 13)"											
XX													
PN	W09807880-A1.												
PD	26-FEB-1998.												
XX													
PE	16-AUG-1996;	96WO-US013282.											
XX													
PR	16-AUG-1996;	96WO-US013282.											
XX													
PA	(HUMA-) HUMAN GENOME SCI INC.												

```
XX  Yu G, Ni J, Rosen CA;
XX  WPI; 1998-169182/15.
DR  N-PSDB; AAV19195.
XX
PT  Nucleic acid encoding human endokine-alpha - useful for diagnosis and
PT  treatment of tumour necrosis factor-related diseases.
XX
PS  Claim 1; Fig 1A-B; 78pp; English.
XX
CC  This polypeptide comprises human endokine-alpha, a novel member of the
CC  tumour necrosis factor (TNF) family of cytokines that shows 30%
CC  similarity and 22% identity to human TNF-alpha. Its amino acid sequence
CC  was deduced from a human striatum cDNA clone (see AAV19195). Isolation of
CC  this nucleic acid allows production of recombinant endokine-alpha
CC  polypeptides in transformed host cells. Endokine-alpha may be involved in
CC  disorders of immunomodulation, infection, cell proliferation,
CC  angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxaemia, and
CC  may be useful for treating melanoma and sarcoma, particularly where
CC  coupled to a radioisotope or cytostatic agent. Antibodies raised against
CC  endokine-alpha are useful diagnostically and for treatment of TNF-
CC  associated disease
XX
SQ  Sequence 169 AA;

Query Match      100.0%; Score 675; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  ETAKPPCAKFGP.LPSKQWASSEPPCVNKYSMDKLETLONGLYLIYGVAPNANYNDVA 60
DB  44  ETAKPPCAKFGP.LPSKQWASSEPPCVNKYSMDKLETLONGLYLIYGVAPNANYNDVA 103
QY  61  PFEVRLYNKMKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB  104  PFEVRLYNKMKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
QY  121  NPQRTS 126
DB  164  NPQRTS 169

RESULT 2
AAB08785
ID  AAB08785 standard; protein, 169 AA.
XX
AC  AAB08785;
XX
DT  02-JAN-2001 (first entry)
XX
DE  A human endokine-alpha polypeptide.
XX
KW  Human; endokine-alpha; cytokine; tumour necrosis factor; TNF; AIDS;
KW  chronic lymphocyte disorder; tumour; parasitic disease; arthritis;
KW  autoimmune disease; lupus; multiple sclerosis; chronic inflammation;
KW  acute inflammation; acute allograft rejection; graft versus host disease;
KW  transplant rejection; foetal resorption; faecal peritonitis; allergy;
KW  bowel disease; sepsis; leukaemia; chronic hypergammaglobulinemia;
KW  polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;
KW  chronic active hepatitis; myasthenia gravis; psoriasis; vitiligo;
KW  Steven-Johnson syndrome; idiopathic sprue; gluten-sensitive enteropathy;
KW  pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;
KW  discoid lupus; dense deposit disease; endocrine ophthalmopathy;
KW  irritable bowel disease; asthma; Grave's disease; sarcoidosis; cirrhosis;
KW  juvenile diabetes; insulin dependent diabetes mellitus; uveitis;
KW  lymphopenias; polyarteritis nodosa; Sjogren's syndrome; Bechet's disease;
KW  primary myxedema; polymyositis; mixed connective tissue disease;
KW  keratoconjunctivitis sicca; vernal keratoconjunctivitis, ss.
XX
OS  Homo sapiens.
XX
FH  Key      Location/Qualifiers
```

```
FT  Domain
FT  1..17
FT  /note= "intracellular domain"
FT  18..43
FT  /note= "transmembrane domain"
FT  44..169
FT  Domain
FT  /note= "extracellular domain"
XX
EN  WO200050620-A2.
XX
PD  31-AUG-2000.
XX
PF  25-FEB-2000; 2000WO-US004722.
XX
PR  26-FEB-1999; 99US-0122099P.
XX  28-MAY-1999; 99US-0136788P.
XX  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Yu G, Ni J, Rosen CA;
XX
DR  WPI; 2000-572097/53.
DR  N-PSDB; AAA74936.
XX
PT  Polynucleotide encoding endokine alpha protein, which is a member of
PT  tumor necrosis factor useful for treating inflammatory diseases,
PT  disorders such as cancer, allergy, diabetes and various neurological
PT  disorders.
XX
PS  Claim 16; Fig 1; 263pp; English.
XX
CC  The present sequence represents a human endokine-alpha polypeptide. The
CC  polypeptide is a cytokine which is similar to tumour necrosis factor
CC  (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
CC  treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
CC  autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
CC  inflammation, acute inflammation, acute allograft rejection, graft versus
CC  host disease, transplant rejection, foetal resorption, faecal
CC  peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
CC  hypergammaglobulinemia, polychondritis, scleroderma, Wegener
CC  granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
CC  gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, vitiligo,
CC  gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
CC  bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
CC  ophthalmopathy, irritable bowel disease, asthma, Grave's disease,
CC  sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
CC  mellitus, uveitis, lymphopenias, polyarteritis nodosa, Sjogren's
CC  syndrome, Bechet's disease, primary myxedema, polymyositis, mixed
CC  connective tissue disease, keratoconjunctivitis sicca, and vernal
CC  keratoconjunctivitis,
XX
SQ  Sequence 169 AA;

Query Match      100.0%; Score 675; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  ETAKPPCAKFGP.LPSKQWASSEPPCVNKYSMDKLETLONGLYLIYGVAPNANYNDVA 60
DB  44  ETAKPPCAKFGP.LPSKQWASSEPPCVNKYSMDKLETLONGLYLIYGVAPNANYNDVA 103
QY  61  PFEVRLYNKMKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB  104  PFEVRLYNKMKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
QY  121  NPQRTS 126
DB  164  NPQRTS 169

RESULT 3
AAV53061
ID  AAV53061 standard; protein, 169 AA.
XX
```

```

AC AAY53061;
XX
XX 03-APR-2000 (first entry)
XX
XX
DE Human endokine alpha protein SEQ ID NO:2.
XX
XX Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
KW immunomodulation; inflammation; cell proliferation; angiogenesis;
XX tumour metastasis; apoptosis; sepsis; endotoxaemia.
XX
OS Homo sapiens.
XX
XX US5998171-A.
XX
XX 07-DEC-1999.
XX
XX 15-AUG-1997; 97US-00912227.
XX
XX 16-AUG-1996; 96US-0024058P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX NI J, Rosen CA, Yu G;
XX
XX WPI; 2000-104608/09.
XX
XX N-PSDB; AAZ57314.
XX
XX
XX Isolated human endokine alpha gene useful as a diagnostic probes and
PT primers.
XX
XX Claim 1; Fig 1; 31pp; English.
XX
XX The present sequence represents human endokine alpha which is a member of
CC the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
CC protein and polynucleotides can be used in diagnostic and therapeutic
CC methods concerning TNF family-related disorders. These include disorders
CC associated with immunomodulation and inflammation, cell proliferation,
CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxaemia
XX
XX Sequence 169 AA;
SQ
Query Match 100.0%; Score 675; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETKPEPCMAKFGPLPSKQWASSEPPCVNKSVDKLEITLNGLYLYGOVAPNANYDVA 60
DB 44 ETKPEPCMAKFGPLPSKQWASSEPPCVNKSVDKLEITLNGLYLYGOVAPNANYDVA 103
QY 61 PFEVRLYKNKDMITQTLTNKSKIQNVGTYELHVGDTIDLI FNSHQVLKNTYWGIIILA 120
DB 104 PFEVRLYKNKDMITQTLTNKSKIQNVGTYELHVGDTIDLI FNSHQVLKNTYWGIIILA 163
QY 121 NPOGIS 126
DB 164 NPOGIS 169

```

RESULT 4
ADAI1464
ID ADAI1464 standard; protein; 169 AA.

AC ADAI1464;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human endokine alpha.
XX
XX human; endokine alpha; melanoma; sarcoma; tumour; tumour regression;
KW infection; viral; bacterial; yeast; fungal; toxoplasma gondii;
KW Schistosoma mansoni; listeria monocytogenes; tumour necrosis factor;
KW TNF-related disorder; endokine alpha-related disorder; immunomodulation;
KW inflammation; cell proliferation; angiogenesis; tumour metastasis;

```

KW apoptosis; sepsis; endotoxaemia.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Domain 1..17
XX Domain /label = Intracellular_domain
XX Domain 18..43
XX Domain /label = Transmembrane_domain
XX Domain 44..169
XX Domain /label = Extracellular_domain
XX
XX US2002099198-A1.
XX
XX 25-JUL-2002.
XX
XX 01-JUL-1999; 99US-00345790.
XX
XX 16-AUG-1996; 96US-0024058P.
XX
XX 15-AUG-1997; 97US-00912227.
XX
XX (YUGG/) YU G.
XX PA (NIJU/) NI J.
XX PA (ROSE/) ROSEN C A.
XX
XX YU G, NI J, Rosen CA;
XX
XX WPI; 2003-605663/57.
XX
XX N-PSDB; ADAI1463.
XX
XX
XX Novel isolated endokine alpha polypeptide, a member of tumor necrosis
PT factor ligand family, and antibodies against the polypeptides, useful for
PT treating melanoma, sarcoma, and viral, bacterial, fungal infections.
XX
XX Claim 16; Fig 1; 29pp; English.
XX
XX The invention relates to an isolated human endokine alpha polypeptide. A
CC cell recombinant for the human endokine alpha polypeptide is useful for
CC producing the protein by recombinant techniques. The antigenic epitope
CC bearing peptides and polypeptides are useful to raise antibodies
CC including monoclonal antibodies. The peptides and antipeptide antibodies
CC are used in a variety of qualitative or quantitative assays for the
CC protein. The protein is useful for tumour targeting and thus used in
CC patients with melanoma and sarcoma for tumour regression and extension of
CC patient life-span through a local injection. The protein is also useful
CC for treating viral, bacterial, yeast, fungal and other infections e.g.,
CC toxoplasma gondii, Schistosoma mansoni, listeria monocytogenes etc. The
CC protein is also useful for treating other tumour necrosis factor (TNF)-
CC related disorders. The nucleic acid is useful as probes for gene mapping
CC by in situ hybridisation and for detecting expression of endokine alpha
CC gene in human tissue e.g. by Northern blot analysis. The nucleic acid is
CC also useful for diagnosing an endokine alpha-related disorder such as
CC disorders associated with immunomodulation and inflammation, cell
CC proliferation, angiogenesis, tumour metastasis, apoptosis, sepsis or
CC endotoxaemia. The antibody is useful diagnostically or therapeutically as
CC antagonists in the treatment of alpha and/or TNF-related disorders. The
CC antibody is also useful for purification of the protein. The antibodies
CC are useful for detecting the protein and for tracking the fate of various
CC regions of a protein precursor which undergoes post-translational
CC processing. The present sequence represents the amino acid sequence of
CC human endokine alpha.
XX
XX Sequence 169 AA;
SQ
Query Match 100.0%; Score 675; DB 6; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETKPEPCMAKFGPLPSKQWASSEPPCVNKSVDKLEITLNGLYLYGOVAPNANYDVA 60
DB 44 ETKPEPCMAKFGPLPSKQWASSEPPCVNKSVDKLEITLNGLYLYGOVAPNANYDVA 103
QY 61 PFEVRLYKNKDMITQTLTNKSKIQNVGTYELHVGDTIDLI FNSHQVLKNTYWGIIILA 120

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Db      104 PEEVALYNKQMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHQVLAKNNTYWGIIILIA 163
QY      121 NPQFIS 126
        |||||
        164 NPQFIS 169

RESULT 5
ADCC01858
ID      ADCC01858 standard; protein; 169 AA.
XX
XX      ADCC01858;
AC
XX      18-DEC-2003 (first entry)
DT
XX
XX      Human Endokine alpha.
DE
XX      Human; endokine alpha; tumour necrosis factor family; AIDS;
KW      chronic lymphocyte disorder; tumour; parasitic disease;
KW      autoimmune disease; lupus; arthritis; multiple sclerosis; inflammation;
KW      graft versus host disease; transplant rejection; skin allergy;
KW      bowel disease; wound; sepsis; Hodgkin's disease;
KW      chronic lymphocyte leukaemia; Burkitt's lymphoma; scleroderma;
KW      chronic active hepatitis; myasthenia gravis; psoriasis;
KW      autoimmune thyroiditis; Goodpasture's disease; asthma; Graves disease;
KW      cirrhosis; insulin dependent diabetes mellitus; Sjogren's syndrome;
KW      glomerulonephritis; hepatitis; Parkinson's disease; atherosclerosis;
KW      rheumatoid arthritis.
XX
XX      Homo sapiens.
OS
XX
XX      Key      Location/Qualifiers
XX      FT      2..169
XX      FT      /note= "This protein is specifically claimed in claim 11"
XX
XX      US2002168729-A1.
XX
XX      14-NOV-2002.
PD
XX
XX      02-MAY-2002; 2002US-00136511.
XX
XX      16-AUG-1996; 96US-0024058P.
XX      PR      15-AUG-1997; 97US-0091222Z.
XX      PR      26-FEB-1999; 99US-0122099Z.
XX      PR      28-MAY-1999; 99US-0136788P.
XX      PR      01-JUL-1999; 99US-00345790.
XX      PR      25-FEB-2000; 2000US-00513584.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
XX
XX      Yu G, Ni J, Rosen CA;
XX
XX      MPI; 2003-755028/71.
XX      DR      N-PSDB; ADCC01857.
XX
XX      Novel isolated endokine alpha polypeptide AIDS, chronic lymphocyte
XX      PT      disorder, common variable immunodeficiency, a tumor, parasitic disease,
XX      PT      autoimmune disease, lupus, arthritis, multiple sclerosis.
XX
XX      Claim 11; SEQ ID NO 2; 90pp; English.
XX
XX      The invention relates to an isolated endokine alpha polypeptide (a member
XX      CC      of the tumour necrosis factor family), appearing as ADCC01858, the
XX      CC      sequence of the endokine alpha polypeptide having an sequence encoded by
XX      CC      the cDNA clone contained in ATCC Deposit number 97640 (A1) and the
XX      CC      sequence of an epitope-bearing portion of the above polypeptides. Also
XX      CC      included are the encoding nucleic acid (its homologues, complements or
XX      CC      fragments where the fragment comprises at least 50 contiguous
XX      CC      nucleotides), provided that the fragment is not from a region starting at
XX      CC      nucleotide 26 and ending at nucleotide 476 of ADCC01857), making a
XX      CC      recombinant vector comprising the nucleic acid and an isolated antibody
XX      CC      or antibody fragment that binds specifically to endokine alpha. The DNA

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CC      and protein are useful for treating an individual having a disorder
CC      CC      chosen from AIDS, chronic lymphocyte disorder, common variable
CC      CC      immunodeficiency, a tumour, parasitic disease, autoimmune disease, lupus,
CC      CC      arthritis, idiopathic thrombocytopenic purpura, multiple sclerosis,
CC      CC      chronic inflammation, acute inflammation, acute allograft rejection,
CC      CC      graft versus host disease, transplant rejection, foetal resorption,
CC      CC      faecal peritonitis, skin allergies, bowel disease, a wound, sepsis, AII,
CC      CC      Hodgkin's disease, non-Hodgkin's lymphoma, chronic lymphocyte leukaemia,
CC      CC      plasmacytoma, multiple myeloma, Burkitt's lymphoma, EBV-transformed
CC      CC      disease, chronic myelogenous leukaemia, chronic hypergammaglobulinaemia,
CC      CC      autoimmune haematological disorders, polychondritis, scleroderma, Wegener
CC      CC      granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
CC      CC      gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, autoimmune
CC      CC      thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive
CC      CC      enteropathy, autoimmune neutropenia, pemphigus vulgaris, Goodpasture's
CC      CC      disease, bullous pemphigoid, discoid lupus, dense deposit disease,
CC      CC      endocrine ophthalmopathy, IBD, asthma, Graves disease, Sarcoidosis,
CC      CC      cirrhosis, juvenile diabetes, insulin dependent diabetes mellitus,
CC      CC      uveitis, autoimmune gastritis, lymphopneumia, oligarteritis nodosa,
CC      CC      Sjogren's syndrome, Bechet's disease, Hashimoto's disease, primary
CC      CC      myxedema, polyomyositis, mixed connective tissue disease, primary
CC      CC      keratoconjunctivitis sicca, vernal keratoconjunctivitis, interstitial
CC      CC      lung fibrosis, glomerulonephritis, hepatitis, autoimmune haemolytic
CC      CC      anaemia, contact sensitivity disease, sarcoidosis, Parkinson's disease, primary
CC      CC      lateral sclerosis, siliocosis, Parkinson's disease, primary
CC      CC      idiopathic hyper-eosinophilic syndrome, endotoxic shock, atherosclerosis,
CC      CC      histamine-mediated allergic reactions, IGE-mediated allergic reactions,
CC      CC      rheumatoid arthritis, plastic anaemia and myelodysplastic syndrome. The
CC      CC      present sequence represents endokine alpha.
XX
XX      SQ      Sequence 169 AA;
XX
XX      Query Match      100.0%; Score 675; DB 7; Length 169;
XX      Best Local Similarity 100.0%; Pred. No. 2.2e-69;
XX      Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 EFAKPPCAKFGPLPSKQWMASSPPCVNKVSDMKLEILQNGLYLYGQVAPNANYNVA 60
XX      |||||
XX      Db      44 EFAKPPCAKFGPLPSKQWMASSPPCVNKVSDMKLEILQNGLYLYGQVAPNANYNVA 103
XX
XX      QY      61 PEEVALYNKQMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHQVLAKNNTYWGIIILIA 120
XX      |||||
XX      Db      104 PEEVALYNKQMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHQVLAKNNTYWGIIILIA 163
XX
XX      QY      121 NPQFIS 126
XX      |||||
XX      Db      164 NPQFIS 169
XX
XX      RESULT 6
XX      AA15817
XX      ID      AA15817 standard; protein; 177 AA.
XX
XX      AA15817;
XX
XX      28-JUL-1999 (first entry)
DT
XX
XX      Amino acid sequence of human DNA19355 polypeptide.
XX
XX      DNA19355; tumour necrosis factor homologue; receptor G1TR; immunogen;
XX      KW      antibody; apoptosis; mammalian cancer cell;
XX      KW      tumour necrosis factor (TNF)-alpha secretion; primary T- cell;
XX      KW      proinflammatory response.
XX
XX      Homo sapiens.
OS
XX
XX      MO9925834-A1.
XX      PN      27-MAY-1999.
XX      PD
XX      18-NOV-1998; 98WO-US024621.
XX      PF
XX      18-NOV-1997; 97US-0065635P.
XX

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PR 12-DEC-1997; 97US-0069661P.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Gurney AL, Marsters SA, Pitti R, Baker KP,
XX Godowski PJ, Mark MR;
XX
XX WPI; 1999-338009/28.
XX N-PSDB; AAX59744.
XX
XX New DNA19355 polypeptide as tumour necrosis factor homolog.
XX
XX Claim 10; Fig 1; 86pp; English.
XX
XX The present sequence represents a polypeptide designated DNA19355. The
XX polypeptide is a tumour necrosis factor homologue. The DNA19355
XX polynucleotide sequence can be used to derive hybridisation probes for
XX e.g. isolating similar sequences, gene mapping, genetic analysis, etc.
XX Nucleic acids which encode DNA19355 can also be used to generate
XX transgenic or knockout animals, which are useful in the development and
XX screening of therapeutically useful reagents. The DNA19355 polypeptides
XX may be used in diagnostic assays to detect the presence of the receptor
XX GTR in mammalian tissues. The polypeptides can also be used as
XX immunogens to raise antibodies. The polypeptides may also be used to
XX induce apoptosis in mammalian cancer cells. DNA19355 polypeptides
XX stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-
XX cells, and so can be used to stimulate a proinflammatory response in
XX mammalian cells
XX
XX Sequence 177 AA:
SQ
Query Match 100.0%; Score 675; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.4e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIAKEPCMAKFGPLPSKQMASSEPPCVNKVSDMKLEILLONGLYLYYGQVAPANANDVA 60
DB 52 EIAKEPCMAKFGPLPSKQMASSEPPCVNKVSDMKLEILLONGLYLYYGQVAPANANDVA 111
QY 61 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNITYWGIITLLA 120
DB 112 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNITYWGIITLLA 171
QY 121 NPOFIS 126
DB 172 NPOFIS 177

RESULT 7
AAY06646
ID AAY06646 standard; protein; 177 AA.
XX
XX AAY06646;
XX
XX 26-OCT-1999 (first entry)
XX
XX Human PRO364 ligand.
XX
XX PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;
XX inflammation; antiinflammatory; NF-KB activation; autoimmune disease;
XX therapy.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH 1..25 "cytoplasmic domain"
XX FT /note="transmembrane domain"
XX FT 26..51
XX FT /note="transmembrane domain"
XX FT 52..177
XX FT /note="extracellular domain"
XX FT Modified-site 129
XX FT /note="N-glycosylation"

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FT Modified-site 161
FT /note="N-glycosylation"
XX
XX W09940196-A1.
XX
XX 12-AUG-1999.
XX
XX 09-FEB-1999; 99MO-US0002642.
XX
XX 09-FEB-1998; 98US-0074087P.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Gurney AL, Marsters SA, Pitti RM, Wood WT,
XX Goddard A,
XX
XX WPI; 1999-494236/41.
XX N-PSDB; AAX87726.
XX
XX Tumor necrosis factor receptor homologue - useful for, e.g. modulating
XX apoptosis and NF-KB activation and proinflammatory or autoimmune
XX responses.
XX
XX Example 2; Fig 5A; 104pp; English.
XX
XX The present sequence represents a putative ligand for PRO364 (see also
XX AAY06605), a novel member of the tumour necrosis factor receptor family.
XX The sequence was deduced from an isolated cDNA clone (see AAX87726).
XX Hypothesis analysis suggests a type II transmembrane homology. The
XX mol.wt. is 20,308. Identity is shown to human Apo-2L (19.8%), Fas/Apo1-
XX ligand (19.0%), TNF-alpha (20.6%) and lymphotoxin-alpha (17.5%). PRO364
XX is useful for modulating apoptosis, NF-KB activation and proinflammatory
XX or autoimmune responses in mammalian cells
XX
XX Sequence 177 AA:
SQ
Query Match 100.0%; Score 675; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.4e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIAKEPCMAKFGPLPSKQMASSEPPCVNKVSDMKLEILLONGLYLYYGQVAPANANDVA 60
DB 52 EIAKEPCMAKFGPLPSKQMASSEPPCVNKVSDMKLEILLONGLYLYYGQVAPANANDVA 111
QY 61 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNITYWGIITLLA 120
DB 112 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNITYWGIITLLA 171
QY 121 NPOFIS 126
DB 172 NPOFIS 177

RESULT 8
AAB47056
ID AAB47056 standard; protein; 177 AA.
XX
XX AAB47056;
XX
XX 08-MAY-2001 (first entry)
XX
XX PRO175.
XX
XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
XX hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;
XX human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
XX myocardial infarction; PGF 2alpha; trauma; cancer; angiogenesis;
XX age-related macular degeneration; antibody; peridontal disease;
XX vascular-related drug targeting; atherosclerosis; hypertension;
XX inflammatory vasculitis; Reynaud's disease; aneurysm;
XX arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
XX fibrosis; neuropathy; rheumatoid arthritis.
XX

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OS Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..25
FT Region /note= "Cytoplasmic region"
FT Region 26..51
FT Region /note= "Transmembrane region"
FT Region 52..177
FT Modified-site 129
FT Modified-site /note= "Extracellular region"
FT Modified-site 161
FT Modified-site /note= "N-glycosylated"
XX WO200103720-A2.
XX 18-JAN-2001.
XX 11-JUL-2000; 2000WO-US018867.
XX 12-JUL-1999; 99US-0143304P.
XX (GETH ) GENENTECH INC.
XX Williams PM, Gerritsen MB;
XX WPI; 2001-138257/14.
XX N-PSDB; AAC85435.
XX Composition for diagnosing and treating cardiovascular, endothelial and
XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
XX Claim 2; Fig 5; 76pp; English.
XX
XX This sequence represents PRO175 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor ligand (hGITRL). The corresponding receptor (hGITR), PRO364, is given in AAB47054. PRO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic agent for the treatment of a cardiovascular, endothelial, angiostatic or angiostatic disorder. The PRO364 sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was isolated from a library of CDNA fragments derived from human umbilical vein endothelial cells (HUVEC). Administering an effective amount of PRO364 or PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF 2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering from a tumor or a retinal disorder. PRO364 or PRO175, or their antagonists, are useful for vascular-related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial stenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis
XX
XX Sequence 177 AA;
XX
XX Query Match 100.0%; Score 675; DB 4; Length 177;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-69;
XX Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 121 NPOFIS 126
DB 172 NPOFIS 177
XX
XX RESULT 9
XX AAB20109
XX ID AAB20109 standard; protein; 177 AA.
XX AC AAB20109;
XX DT 30-APR-2001 (first entry)
XX
XX Human immunostimulant PRO175.
XX
XX PRO175; UNQ149; human, immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antihypertoid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic; anti allergic; immunostimulant.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..44
FT Peptide /label= Signal_peptide
FT Modified-site 18..24
FT Modified-site /note= "N-myristoylation site"
FT Protein 45..177
FT Modified-site /label= Mature_protein
FT Modified-site 129..133
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 161..165
FT Modified-site /note= "Asn is N-glycosylated"
XX
XX WO200105972-A1.
XX 25-JAN-2001.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-JUL-1999; 99US-0144758P.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ,
XX Gurney AL, Hillan KJ, Mark MK, Marsters SA, Pitti RM, Tumas D;
XX Watanabe CK, Wood WI;
XX WPI; 2001-103149/11.
XX N-PSDB; AAF30051.
XX
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for
XX diagnosing and treating immune-related disorders, such as multiple
XX sclerosis, rheumatoid arthritis and diabetes.
XX Claim 20; Fig 4; 127pp; English.
XX
XX The present sequence is that of PRO175 (UNQ149), a novel human
XX immunomodulator protein (20 kDa, pI 8.08) showing homology to tumour
XX necrosis factor family members. The invention provides polynucleotides
XX (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)
XX including PRO175. Claimed compositions comprising these proteins or their
XX agonists are useful for increasing infiltration of inflammatory cells
XX into a tissue of a mammal, stimulating or enhancing an immune response in
XX a mammal, or increasing the proliferation of T-lymphocytes in a mammal in
XX response to an antigen. Claimed compositions comprising the PRO
XX polypeptide or its antagonist have the opposite effect. A claimed method
XX for treating an immune related disorder, such as a T cell disorder,
XX involves administering the PRO polypeptide, an agonist antibody or an
XX antineoplastic agent. The disorder is selected from systemic lupus
XX erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
```

CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune hemolytic anaemia, autoimmune thrombocytopenia,
 CC thyroditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinated diseases (such as multiple sclerosis), autoimmune chronic
 CC active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,
 CC sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis
 CC and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,
 CC (auto) immune-mediated skin diseases (such as bullous skin disease,
 CC erythema multiforme and psoriasis), allergic diseases (such as asthma,
 CC urticaria), immunologic diseases of the lung and transplantation
 CC associated diseases (such as graft rejection and graft-versus-host
 CC disease) (all claimed). Claimed methods of diagnosing these disorders
 CC comprise detecting the level of expression of the PRO gene. Also claimed
 CC are a method of identifying a compound capable of inhibiting the
 CC expression or activity of the PRO polypeptide, vectors, host cells,
 CC antibodies, and a method of stimulating an immune response in a mammal
 CC using PRO179
 XX
 SQ Sequence 177 AA;

Query Match 100.0%; Score 675; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.4e-69;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPECMAKFGPLPSKQMASSEPPCVNKVSDMKLEILONGYLITYGQVAPNANNVDA 60
 DB 52 ETAKPECMAKFGPLPSKQMASSEPPCVNKVSDMKLEILONGYLITYGQVAPNANNVDA 111
 QY 61 PFEVRLYNKMDIQTITNKSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 120
 DB 112 PFEVRLYNKMDIQTITNKSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 171
 QY 121 NPQFIS 126
 DB 172 NPQFIS 177

RESULT 10
 AAB53065
 ID AAB53065 standard; protein; 177 AA.

AC AAB53065;
 DT 28-FEB-2001 (first entry)
 DE Human angiogenesis-associated protein PRO175, SEQ ID NO:9.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US000219.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 XX
 PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Peoni NF, Pletti RM, Watanabe CK, Williams PM, Wood WT;
 DR WPI; 2001-090793/10.
 DR N-PSDB; AAC97374.

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic
 PT disorders, such as atherosclerosis, wounds or cancer.

PS Claim 69; Fig 4; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to screen
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals
 CC useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a PRO protein of the invention
 XX
 SQ Sequence 177 AA;

Query Match 100.0%; Score 675; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.4e-69;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPECMAKFGPLPSKQMASSEPPCVNKVSDMKLEILONGYLITYGQVAPNANNVDA 60
 DB 52 ETAKPECMAKFGPLPSKQMASSEPPCVNKVSDMKLEILONGYLITYGQVAPNANNVDA 111
 QY 61 PFEVRLYNKMDIQTITNKSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 120
 DB 112 PFEVRLYNKMDIQTITNKSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 171
 QY 121 NPQFIS 126
 DB 172 NPQFIS 177

CC	AAAB47287	standard; protein; 177 AA.
XX	AAAB47287	
XX	AAAB47287	
DT	22-AUG-2001	(first entry)
XX		
DE	PRO175 polypeptide.	
XX		
KW	PRO; type II transmembrane protein; tumour necrosis factor; stroke;	
KW	heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;	
KW	myocardial infarction; cardiac hypertrophy; PGF 2alpha; trauma; bone;	
KW	cancer; age-related macular degeneration; wound; burn; hypertension;	
KW	diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; amyotrophic lateral sclerosis;	
KW	endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;	
XX	Alzheimer's disease; Parkinson's disease; Huntington's disease.	
XX		
OS	Homo sapiens.	
FH		
FT	Key	Location/Qualifiers
FT	Peptide	1..25
FT		/label= Signal peptide
FT		18..24
FT	Modified-site	/label= N-myristoylation site
FT		26..177
FT	Protein	/label= Mature PRO175
FT		26..51
FT	Domain	/label= Transmembrane domain
FT		52..177
FT	Domain	/label= Extracellular domain
FT		129..133
FT	Modified-site	/label= N-linked glycosylation site
FT		161..165
FT	Modified-site	/label= N-linked glycosylation site
FT		
XX		
PN	WO200140464-A1.	
XX		
XX		
PD	07-JUN-2001.	
XX		
XX	11-AUG-2000; 2000WO-US022031.	
XX		
PR	30-NOV-1999; 99WO-US028313.	
PR	30-NOV-1999; 99WO-US028409.	
PR	05-JAN-2000; 2000WO-US000219.	
PR	24-FEB-2000; 2000WO-US005004.	
PR	15-MAR-2000; 2000WO-US006884.	
PR	30-MAR-2000; 2000WO-US006439.	
PR	17-MAY-2000; 2000WO-US013705.	
PR	30-MAY-2000; 2000WO-US014941.	
PR	28-JUL-2000; 2000WO-US020710.	
XX		
PA	(GETH) GENENTECH INC.	
PI	Ashkenazi AJ, Baker KP, Ferrara N, Godowski PC, Gurney AJ;	
PI	Hillan KJ, Mark MR, Marsters SA, Paoni NF, Pitti RM, Wood WJ;	
XX		
DR	WPI, 2001-361383/40.	
XX		
XX	N-PSDB; AAC85945.	
PT		
PT	isolated PRO polypeptide useful in treating and diagnosing a	
PT	cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes	
PT	mellitus, myocardial infarction, arthritis.	
XX		
PS	Claim 56; Fig 2; 144pp; English.	
XX		
CC	The sequences given in AAAB47287-90 show PRO polypeptides. PRO175 shows	
CC	type II transmembrane protein typology, and portions of PRO364 show	
CC	homology to members of the tumour necrosis factor (TNF) family, thereby	
CC	indicating that it may be a novel member of the TNF family. PRO175 and	
CC	PRO168 stimulated heat hypertrophy. PRO CDNA's may be used to identify a	

CC	compound that inhibits PRO, diagnosing a cardio-vascular, endothelial or
CC	angiogenic disorder in a mammal by detecting PRO cDNA, treating
CC	cardiovascular, endothelial or angiogenic disorder in a mammal, and
CC	inducing cardiac hypertrophy or inhibiting endothelial cell growth or
CC	angiogenesis in a mammal. The mammal is a human which has suffered
CC	myocardial infarction, cardiac hypertrophy characterized by the presence
CC	of elevated PGE ₂ /alpha, trauma, cancer or age-related macular
CC	dysgenesis. Trauma includes wounds or burns. Other treatable diseases
CC	include diabetes mellitus, osteoporosis, ischemia, hyper-tension,
CC	rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,
CC	endometriosis, angina, neoplasms, periodontal disease, bone and cartilage
CC	repair, Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC	amyotrophic lateral sclerosis, and stroke
XX	
SQ	Sequence 177 AA;
Query Match	100.0%; Score 675; DB 4; Length 177;
Best Local Similarity	100.0%; Pred. No. 2,4e-69;
Matches 126; Conservative	0; Mismatches 0; Indels 0
	Gaps 0
QY	1 ETAKEPCKAKGCPSPSKWOMASSPEPCCNKYSDMKLTLONGCLYLITGVAPNANYNDA 60
DB	52 ETAKEPPCAKGPLPSKWKOMASSPEPCCNKYSDMKLTLONGCLYLITGVAPNANYNDA 111
QY	61 PFEEVLYLNKKMIQTLLTNKSKIQNVGTYELHVGDTIDLINSEHQVLKNNTYWGIIILA 120
DB	112 PFEEVLYLNKKMIOQLLTNKSKIQNVGTYELHVGDTIDLINSEHQVLKNNTYWGIIILA 171
QY	121 NPOFTS 126
DB	172 NPOFTS 177

RESULT 12	
AAB50979	
ID	AAB50979 standard; protein; 177 AA.
XX	
AC	
XX	AAB50979;
DT	21-MAR-2001 (first entry)
XX	
DE	Human PRO175 protein.
XX	
KW	Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;
KW	vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
KW	vulnerary; antianginal; gene therapy; cardiovascular disease;
KW	endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW	wound healing.
XX	
OS	Homo sapiens.
XX	
PN	WO200073445-A2.
XX	
PD	07-DEC-2000.
XX	
PF	17-MAY-2000; 2000OWO-US013705.
XX	
PR	02-JUN-1999; 99WO-US012252.
PR	23-JUN-1999; 99US-0141037P.
PR	20-JUL-1999; 99US-0144758P.
PR	26-JUL-1999; 99US-0145698P.
PR	28-JUL-1999; 99US-0146222P.
PR	01-SEP-1999; 99WO-US020111.
PR	30-NOV-1999; 99WO-US028313.
PR	30-NOV-1999; 99WO-US028409.
PR	02-DEC-1999; 99WO-US028565.
PR	16-DEC-1999; 99WO-US030095.
PR	05-JAN-2000; 2000OWO-US000219.
PR	06-JAN-2000; 2000OWO-US000376.
PR	11-FEB-2000; 2000OWO-US003565.
PR	18-FEB-2000; 2000OWO-US004341.
PR	18-FEB-2000; 2000OWO-US004342.
PR	24-FEB-2000; 2000OWO-US005004.

02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertsen ME;
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI: 2001-025251/03.
 DR N-PSDB; AAC90563.
 XX
 PT Seventeen nucleic acids encoding PRO polypeptides which are useful in
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic
 PT disorders in a mammal.
 XX
 PS Claim 71; Fig 2; 182pp; English.
 XX
 CC The present sequence is one of seventeen novel PRO polypeptides. The PRO
 CC nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and
 CC antagonists are also used to prevent tumour angiogenesis and for treating
 CC periodontal diseases. They are also used to stimulate wound healing and
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder
 XX
 SQ Sequence 177 AA;
 Query Match 100.0%; Score 675; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.4e-69;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ETKAEPCMAKFGPLPSKQMASSEPPCVNKSVDWKLTLIQLNGLYLYIGVAPNANNVNDVA 60
 Db 52 ETKAEPCMAKFGPLPSKQMASSEPPCVNKSVDWKLTLIQLNGLYLYIGVAPNANNVNDVA 111
 QY 61 PEEVRLYKXKMDIQLTLNKSQIQNVGTYELAHVDTIDILFNEHQVLLKNNTYWGIIILA 120
 Db 112 PEEVRLYKXKMDIQLTLNKSQIQNVGTYELAHVDTIDILFNEHQVLLKNNTYWGIIILA 171
 QY 121 NQOFIS 126
 Db 172 NQOFIS 177
 Db
 RESULT 13
 AAU81953
 ID AAU81953 standard; protein; 177 AA.
 XX
 AC AAU81953;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human PRO175.
 XX
 KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;
 KW retinal cell injury; ocular disease; retinitis pigmentosa;
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;
 KW retinal degenerative disease; macular hole; degenerative myopia;
 KW acute retinal necrosis syndrome; traumatic chorioretinopathy;
 KW Purtscher's retinopathy; oedema; ischaemic condition;
 KW retinal vision occlusion; collagen vascular disease;
 KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;
 KW systemic lupus erythematosus; environmental trauma.

OS Homo sapiens.
 XX
 EN WO200109327-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-US020710.
 XX
 PR 28-JUL-1999; 99US-0146222P.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;
 PI KJavan IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM, Watanabe CK;
 PI Wood WI;
 XX
 DR WPI: 2002-130120/17.
 DR N-PSDB; ABK28562.
 XX
 PT Promoting survival of retinal cells, or delaying or preventing retinal
 PT cell injury or death, by contacting retinal cells with PRO175, 220, 216,
 PT 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132 polypeptide.
 XX
 PS Claim 44; Fig 2; 152pp; English.
 XX
 CC The invention relates to promoting the survival of retinal cells, or
 CC delaying or preventing retinal cell injury or death, by contacting the
 CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,
 CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO826, PRO826,
 CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids
 CC encoding the PRO proteins, a vector comprising the nucleic acid, a host
 CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are
 CC useful for promoting survival of retinal cells (retinal neurons such as
 CC retinal ganglion cells, displaced retinal ganglion cells, amacrine cells,
 CC displaced amacrine cells, horizontal neurons or bipolar neurons, rod
 CC photoreceptors, or supportive cells such as Muller cells or pigment
 CC epithelial cells), or delaying or preventing retinal cell injury or death
 CC caused by ocular disease (which is or is associated with retinitis
 CC pigmentosa, macular degeneration, retinal detachment, retinal tear,
 CC retinopathy, retinal degenerative disease, macular hole, degenerative
 CC myopia, acute retinal necrosis syndrome, traumatic chorioretinopathy or
 CC contusion, Purtscher's retinopathy, oedema, an ischaemic condition,
 CC central or branch retinal vision occlusion, collagen vascular disease,
 CC thrombocytopaenic purpura, uveitis, retinal vasculitis, occlusion
 CC associated with Bales disease or systemic lupus erythematosus), retinal
 CC injury or environmental trauma. The retinal cell injury or death is
 CC delayed or prevented by substantially not causing angiogenesis or
 CC mitogenesis. The present sequence represents a PRO protein
 XX
 SQ Sequence 177 AA;
 Query Match 100.0%; Score 675; DB 5; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.4e-69;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ETKAEPCMAKFGPLPSKQMASSEPPCVNKSVDWKLTLIQLNGLYLYIGVAPNANNVNDVA 60
 Db 52 ETKAEPCMAKFGPLPSKQMASSEPPCVNKSVDWKLTLIQLNGLYLYIGVAPNANNVNDVA 111

QY 61 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHQVLYKKNYTWGIIILLA 120
| | | | |
Db 112 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHQVLYKKNYTWGIIILLA 171
| | | | |
QY 121 NPOFIS 126
| | | | |
Db 172 NPOFIS 177
| | | | |

RESULT 14
ABR42323 standard; protein; 177 AA.
ID ABR42323
XX ABR42323;
AC
XX
XX 11-AUG-2003 (first entry)
DT
XX Human GITRL protein.
DB
XX Human GITRL; tumour necrosis factor; ligand; cytostatic;
KM immunomodulator; osteopathic.
KW
XX Homo sapiens.
OS
XX WO2003040307-A2.
PN
XX 15-MAY-2003.
PD
XX 25-JUL-2002; 2002WO-US023782.
PF
XX 27-JUL-2001; 2001US-0307838P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Hilbert DE, Rosen CA;
PI
XX WPI; 2003-430659/40.
DR N-PSDB; ACC57909.
XX
XX New heteromultimeric complex having a first polypeptide member of the
PT tumour necrosis factor (TNF) ligand family, and a second different member
PT of TNF ligand family, useful for treating cancer, osteoporosis or an
PT autoimmune disease.
PS
XX Disclosure; Page 382-383; 388pp; English.

CC The invention relates to the protein sequence of human GITRL polypeptide.
CC The invention relates to compositions comprising heterotrimeric complexes
CC of tumour necrosis factor (TNF) ligand family members, and their use in
CC the detection, prevention and treatment of disease. In preferred
CC embodiments, the heterotrimeric complex comprises full-length or
CC extracellular portions of GITRL together with full-length or
CC extracellular portions of other TNF ligand family members. The
CC heterotrimeric complexes of the invention are useful for treating an
CC autoimmune disease, cancer or osteoporosis, and particularly for
CC inhibiting cancer cell proliferation, increasing B cell proliferation, or
CC inducing apoptosis of T cells

QY 100.0%; Score 675; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.4e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKAPECKAKFGPILPSKQWMASSPEPCVANKVSDMKLEIIQNGIYLLYGVVAPNANYNDVA 60
| | | | |
Db 52 ETKAPECKAKFGPILPSKQWMASSPEPCVANKVSDMKLEIIQNGIYLLYGVVAPNANYNDVA 111
| | | | |
QY 61 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHQVLYKKNYTWGIIILLA 120
| | | | |
Db 112 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHQVLYKKNYTWGIIILLA 171
| | | | |

QY 121 NPOFIS 126
| | | | |
Db 172 NPOFIS 177
| | | | |

RESULT 15
ABP60544 standard; protein; 177 AA.
ID ABP60544
XX ABP60544;
AC
XX 28-MAR-2003 (first entry)
DT
XX Human tumour necrosis factor endokine-alpha.
DE
XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
KW dermatological; immunosuppressive; antiinflammatory; antineumatic;
KW antiarthritic; cytostatic; antianaemic; antiallergic; antiaesthetic;
KW neuroprotective; ophthalmological; tuberculosstatic; antidiabetic;
KW antiporiatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
KW inflammatory disorder; proliferative disorder; single chain antibody;
KW antibody; human; tumour necrosis factor; endokine-alpha.
XX
XX Homo sapiens.
OS
XX WO200294192-A2.
PN
XX 28-NOV-2002.
PD
XX 22-MAY-2002; 2002WO-US016106.
PF
XX 24-MAY-2001; 2001US-0293100P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM;
PI
XX WPI; 2003-156746/15.
DR
XX Novel isolated antibody that immunospecifically binds tumor necrosis
PT factor delta, useful for treating, preventing or ameliorating Non-
PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
PT syndrome.
PS
XX Disclosure; Page 214-215; 225pp; English.

CC The invention relates to a novel antibody or its fragment, which
CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
CC The antibody of the invention has dermatological, immunosuppressive,
CC antiinflammatory, antineumatic, antiarthritic, cytostatic, antianaemic,
CC antiallergic, antiaesthetic, neuroprotective, ophthalmological,
CC tuberculosstatic, antidiabetic, antiporiatic, anti-HIV,
CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
CC The antibody or its fragment are useful for treating, preventing or
CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
CC human, disease or disorder such as autoimmune disease, and graft versus
CC host disease (GVHD). The autoimmune disease is systemic lupus
CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
CC is useful for detecting, diagnosing, prognosing, treating, preventing or
CC ameliorating a disease or disorder associated with aberrant APRIL or
CC APRIL receptor expression or aberrant function of APRIL or APRIL
CC receptor. The disease or disorders includes autoimmune anaemia, dermatitis,
CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
CC system, particularly B cell cancers, immune disorders such as myasthenia
CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
CC proliferative disorders (e.g. leukemia). The present sequence represents
CC the tumour necrosis factor endokine-alpha

QY Sequence 177 AA;

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Query Match      100.0%; Score 675; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 2,4e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1  ETAKPCMAKFGPIPSKQWMASSPEPCVNVSDWKLEITLQNGLYLIYGQVAPNANVNDVA 60
    |||
Db 52  ETAKPCMAKFGPLPSKQWMASSPEPCVNVSDWKLEITLQNGLYLIYGQVAPNANVNDVA 111
    |||

QY 61  PFEVRLYKNKDMIQTLTNKSKIQNVGTYELHVGDTIDLPNSEHQVLKNTYWGIIILA 120
    |||
Db 112  PFEVRLYKNKDMIQTLTNKSKIQNVGTYELHVGDTIDLPNSEHQVLKNTYWGIIILA 171
    |||

QY 121  NPQFIS 126
    |||
Db 172  NPQFIS 177
    |||

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Search Completed: November 2, 2004, 12:55:27
 Job time : 157 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 12:50:37 ; Search time 39 Seconds
(without alignments)
214.258 Million cell updates/sec

Title: US-10-080-455-1_COPY_52_177

Perfect score: 675
Sequence: 1 ETKKEPCMAKFGPLPSKWMQ.....VLKNNTYGIILLNPQFIS 126

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/prodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/aa/PCtUS.COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	169	2	US-08-912-227-2
2	675	100.0	169	4	US-09-513-584-2
3	675	100.0	169	4	US-09-345-790-2
4	84.5	12.5	1221	4	US-09-107-532A-3959
5	77	11.4	217	4	US-09-248-796A-20671
6	76	11.3	2763	3	US-08-496-944-2
7	74	11.0	157	5	PCT-US93-02475-6
8	74	11.0	235	4	US-09-270-767-49088
9	74	11.0	543	3	US-08-697-610-2
10	74	11.0	543	3	US-09-645-926A-7
11	74	11.0	567	4	US-09-645-926A-7
12	73	10.8	289	4	US-09-248-796A-15058
13	72	10.7	609	4	US-09-396-149-6
14	71	10.5	157	5	PCT-US93-02475-2
15	71	10.5	620	4	US-09-710-879-606
16	71	10.5	621	4	US-09-710-879-606
17	71	10.5	680	4	US-09-583-110-3191
18	70.5	10.4	396	4	US-09-248-796A-19923
19	70	10.4	157	5	PCT-US93-02475-7
20	70	10.4	641	4	US-09-248-796A-17974
21	69.5	10.3	211	4	US-09-322-409-78
22	69.5	10.3	211	4	US-09-451-527-78
23	69.5	10.3	235	4	US-09-131-237C-7
24	69.5	10.3	260	4	US-09-322-409-73
25	69.5	10.3	260	4	US-09-451-527-73
26	69.5	10.3	422	4	US-09-270-767-42572
27	69.5	10.3	964	1	US-08-257-073-3

28	69.5	10.3	984	2	US-08-184-009-120	Sequence 120, App
29	69.5	10.3	984	2	US-08-458-356-120	Sequence 120, App
30	69.5	10.3	984	3	US-08-460-736-120	Sequence 120, App
31	69.5	10.3	984	4	US-09-535-370-120	Sequence 120, App
32	69.5	10.3	984	4	US-09-663-667-120	Sequence 120, App
33	69.5	10.3	984	3	US-08-213-419B-2	Sequence 2, Appl
34	69.5	10.3	984	3	US-08-213-419B-2	Sequence 2, Appl
35	69.5	10.3	1013	4	US-09-255-829-18	Sequence 18, Appl
36	69	10.2	634	4	US-09-543-681A-7019	Sequence 7019, Ap
37	68.5	10.1	1604	3	US-09-004-838-95	Sequence 95, Appl
38	68.5	10.1	3443	2	US-08-416-603-2	Sequence 2, Appl
39	68.5	10.1	3623	4	US-09-341-461-2	Sequence 2, Appl
40	68	10.1	487	4	US-09-248-796A-16516	Sequence 16516, A
41	67.5	10.0	211	4	US-09-322-409-70	Sequence 70, Appl
42	67.5	10.0	211	4	US-09-451-527-70	Sequence 70, Appl
43	67.5	10.0	260	4	US-09-322-409-65	Sequence 65, Appl
44	67.5	10.0	260	4	US-09-451-527-65	Sequence 65, Appl
45	67.5	10.0	289	4	US-09-589-287B-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-08-912-227-2
Sequence 2, Application US/08912227
Patent No. 5998171
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,227
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,058
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0470001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-227-2

Query Match 100.0%; Score 675; DB 2; Length 169;
Best local Similarity 100.0%; Pred. No. 2.2e-75;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ETKKEPCMAKFGPLPSKWMASSEPCNKVSDMKLEILLONGLYLTYGVAPNANYNDVA 60
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Db 44 ETRAKPCMAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 120
Db 104 PFEVRLYNKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 163
QY 121 NPQFIS 126
Db 164 NPQFIS 169

RESULT 2

US-09-513-584-2
; Sequence 2, Application US/09513584
; Patent No. 6406867
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha and Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,
; ADDRESS: P.L.I.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/513,584
; FILING DATE: 25-FEB-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,058
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,227
; FILING DATE: 15-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/122,099
; FILING DATE: 26-FEB-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/136,788
; FILING DATE: 28-MAY-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/345,790
; FILING DATE: 01-JUL-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-513-584-2

Query Match 100.0%; Score 675; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-75;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETRAKPCMAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 60
Db 44 ETRAKPCMAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 120
Db 104 PFEVRLYNKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 163
QY 121 NPQFIS 126
Db 164 NPQFIS 169

RESULT 3

US-09-345-790-2
; Sequence 2, Application US/09345790
; Patent No. 6521742
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.I.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,790
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,227
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-345-790-2

Query Match 100.0%; Score 675; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-75;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETRAKPCMAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 60
Db 44 ETRAKPCMAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 120
Db 104 PFEVRLYNKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 163
QY 121 NPQFIS 126
Db 164 NPQFIS 169

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FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20671
LENGTH: 217
TYPE: PRF
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (15)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are
US-09-248-796A-20671

Query Match      11.4%; Score 77; DB 4; Length 217;
Best Local Similarity 27.2%; Pred. No. 0.3;
Matches 31; Conservative 13; Mismatches 44; Indels 26; Gaps 7;

CY      15 PSKMQMASS--EPP-----CVNKSVDWKLFTLQGLYITGYQVAP---NNYNDVAPF 62
Db      85 PKDWDADAKQWEPEPLIVMPKCATGCGPWEALPIPHNDYL--GPWFPPDLIKENYNIGI--W 140
          ||| | | | | | | | | | : | | | | | | | | | | | | | | | | | | | |
CY      63 EVRLYKNKOMTQLTLTKSKIQNVGT-YELHVGDTIDLIENSEHOVLKNNITYWG 115
Db     141 TPRLIPNDYYQVKTPGKLDXPIGIGIFEL-----WSIESILFDNIYILG 185
          ||| | | | | | | | | | : | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-08-496-944-2
Sequence 2, Application US/08496944
Patent No. 6040496
GENERAL INFORMATION:
APPLICANT: Law, Marcus D
TITLE OF INVENTION: Dietz, Jon M
TITLE OF INVENTION: Use of translationally altered RNA to
TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESS: CIBA-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,944
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1814
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-496-944-2

Query Match      11.3%; Score 76; DB 3; Length 2763;
Best Local Similarity 25.8%; Pred. No. 17;
Matches 31; Conservative 18; Mismatches 51; Indels 20; Gaps 5;

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QY 4 KEECAKKEPPELSSKOMASSEPPCNKATXMDKLTQNGELIYQVAPANNVYDAPFE 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 22 KERCNPKESHLTLMQVAFETICHTYDNGSKQIMV-SPALIKVNTLPDPDAMKASALLE 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 64 V-RLYK-NK-----DMICLTITKSKIQNVGVGYELHVDITDLFNSHQVLYK-NYWG 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 81 VSMYNNKRESLEKTLDSLEFNK-----ISPSTINAAIMCDNDQKRIANVWG 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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1      RESULT 7
2      PCT-US93-02475-6
3      Sequence 6, Application PC/TUS9302475
4      GENERAL INFORMATION:
5      APPLICANT: Wisnieski, Bernadine J.
6      TITLE OF INVENTION: Tumor Necrosis Factor with Modified
7      TITLE OF INVENTION: Ion Channel
8      NUMBER OF SEQUENCES: 13
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Donald G. Lewis
11     STREET: 8328 Regents Road #1B
12     CITY: San Diego
13     STATE: California
14     COUNTRY: USA
15     ZIP: 92122
16     COMPUTER READABLE FORM:
17     MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage
18     COMPUTER: VE System 386
19     OPERATING SYSTEM: MS-DOS 5
20     SOFTWARE: Word Perfect
21     CURRENT APPLICATION DATA:
22     APPLICATION NUMBER: PCT/US93/02475
23     FILING DATE: 19930412
24     CLASSIFICATION:
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: US 07/852,625
27     FILING DATE: 12 March 1992
28     ATTORNEY/AGENT INFORMATION:
29     NAME: Donald G. Lewis
30     REGISTRATION NUMBER: 28636
31     REFERENCE/DOCKET NUMBER: BUW-2
32     TELECOMMUNICATION INFORMATION:
33     TELEPHONE: (619) 554-2421
34     TELEFAX: (619) 554-6312
35     INFORMATION FOR SEQ ID NO: 6:
36     SEQUENCE CHARACTERISTICS:
37     LENGTH: 157 amino acids
38     TYPE: AMINO ACIDS
39     TOPOLOGY: linear
40     MOLECULE TYPE: protein
41     FEATURE:
42     NAME/KEY: Tumor Necrosis Factor (feline)
43     PUBLICATION INFORMATION:
44     AUTHORS: McGraw, R. A., Coffee, B.W., Otto,
45     AUTHORS: C.M., Drews, R.T., and Rawling, C.A.
46     TITLE: Gene Sequence of Feline Tumor Necrosis
47     TITLE: Factor
48     JOURNAL: Nucleic Acids Research
49     VOLUME: 18
50     PAGES: 5564
51     DATE: 1990
52     RELEVANT RESIDUES IN SEQ ID NO: 6: 1-157
53     PCT-US93-02475-6

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```

Query Match      11.0% Score 74; DB 5; length 157;
Beet local similarity 24.4%; Pred. No. 0.45;
Matches 30; Conservative 21; Mismatches 32; Indels 40; Gaps

QY      30 KVSPPKELIENGLYLYIGV-----APNANY---NDVAFEPYRLKXKMDIQTLLNS 80
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
Db      42 ELLTNQLKVPDGYLYIYSQVLFTGGCCPSTHVLTHAIRFVNSQTKXNLSAI--KS 99
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::

QY      81 KION-----VGGTELEHVDPTD-----LIENSEHQLKNNTYWG 11

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Db 100 PCQRRTPEGAAKPMVEPIYLGAVFQLEKGRPLSTETNLPAYLDFASSGVY----YFGI 154
Qy 117 ILL 119
Db 155 IAL 157

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RESULT 8
US-09-270-767-49088
; Sequence 49088, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49088
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-49088

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Query Match	11.0%;	Score 74;	DB 4;	Length 235;
Best Local Similarity	32.4%;	Pred. No. 0.81;		
Matches	33;	Conservative	10;	Mismatches 31;
				Indels 28;
				Gaps 77.

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QY 3 KLEIILONGIYIIVGOV--APNANY--NDV-----APEVRLYKKKMDIQTILNK 78
Db 20 KLEPLKE-LMKIKSQVSSARNAYRFPDIPDQYHARHMAQAEYERQSKKE-----TKT 73
QY 80 SKIONVGSTY-----ELAVGDT-IDLIENSHEQVKNNTYM 114
Db 74 KEFQYNGKAEALQESHIIIDIPVDJFNKDSHVVILITAM 115

```

RESULT 9
 ; Sequence 2, Application US/08697610
 ; Patent No. 6172187
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; APPLICANT: Sato, Takaki
 ; TITLE OF INVENTION: CD40 Associated Proteins
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/697,610
 ;
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/349,357
 ;
 ; FILING DATE: 02-DEC-1994
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IJ 1203
 ;
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-697-610-2

Query Match 11.0%; Score 74; DB 3; Length 543;
Best Local Similarity 28.3%; Pred. No. 2.7;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPPCVNKSVDW-----KLEILONGLYLYGVAPNAN---YNDVAPFEVRLYK 70
DB 228 ASSAVGHVNLKEMSNLSLEKVSILQN-----ESVEKNKSISQSLNHQICSFELIEROK 281

QY 71 DMIQTLNKSQIONVGTYELHVGDTIDLIENSEHQVLK 109
DB 282 EMLR--NNESKI-----LHQRVID---SQAEKTK 306

RESULT 10

US-08-349-357-2
Sequence 2, Application US/08349357
Patent No. 6265556
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: CD40 Associated Proteins
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,357
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-349-357-2

Query Match 11.0%; Score 74; DB 3; Length 543;
Best Local Similarity 28.3%; Pred. No. 2.7;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPPCVNKSVDW-----KLEILONGLYLYGVAPNAN---YNDVAPFEVRLYK 70
DB 228 ASSAVGHVNLKEMSNLSLEKVSILQN-----ESVEKNKSISQSLNHQICSFELIEROK 281

QY 71 DMIQTLNKSQIONVGTYELHVGDTIDLIENSEHQVLK 109
DB 282 EMLR--NNESKI-----LHQRVID---SQAEKTK 306

RESULT 11

US-09-645-926A-7
Sequence 7, Application US/09645926A
Patent No. 6482411
GENERAL INFORMATION:
APPLICANT: AHUJA, SEEMA
APPLICANT: BONEWALD, LYNDIA
TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4003.001000
CURRENT APPLICATION NUMBER: US/09/645,926A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/151,250
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 567
TYPE: PRT
ORGANISM: Homo sapiens
US-09-645-926A-7

Query Match 11.0%; Score 74; DB 4; Length 567;
Best Local Similarity 28.3%; Pred. No. 2.9;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPPCVNKSVDW-----KLEILONGLYLYGVAPNAN---YNDVAPFEVRLYK 70
DB 252 ASSAVGHVNLKEMSNLSLEKVSILQN-----ESVEKNKSISQSLNHQICSFELIEROK 305

QY 71 DMIQTLNKSQIONVGTYELHVGDTIDLIENSEHQVLK 109
DB 306 EMLR--NNESKI-----LHQRVID---SQAEKTK 330

RESULT 12

US-09-248-796A-15058
Sequence 15058, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15058
LENGTH: 289
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-15058

Query Match 10.8%; Score 73; DB 4; Length 289;
Best Local Similarity 22.7%; Pred. No. 1.4;
Matches 30; Conservative 23; Mismatches 37; Indels 42; Gaps 6;

QY 20 MASSEPPCVNKSVDWLEILIQ--NGLYLYGVAPNANVNDVAPFEVRLY-----KN 69
DB 143 IAINKSSISLADLKYQVYIPYFNGIY-----NPTSSYVRLPKFSIPKYGTSSEVNPPI 196

QY 70 KMIQTLNKSQ--IONV-----GTYELHVGDTIDLIENSEHQVLK 113
DB 197 KRSIHRTLNNYKFFQVNIKTEADKYHMLTIRANTTKRIQYIYKSLFYNSE-----247

QY 114 WGIILLANPQFI 125
DB 248 -GILARRNDIFM 258

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RESULT 13
US-09-396-149-6
; Sequence 6, Application US/09396149
; Patent No. 6518176
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize Replication Protein A and Use
; FILE REFERENCE: 5718-59
; CURRENT APPLICATION NUMBER: US/09/396,149
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-396-149-6

Query Match          10.7%; Score 72; DB 4; Length 609;
Best Local Similarity 24.3%; Pred. No. 5.7;
Matches 36; Conservative 25; Mismatches 51; Indels 36; Gaps 9;

QY 3 AKPCMAKFGPLSPKQWASSEPCVKNKVDWKLEILLNGLYLYIGQV---PVANYND 58
DB 127 AAPAPASAP-AAPAPSKLQNNASAPPSPMNR-----GTSKLFGGSLNTPGGSQSK 174
QY 59 VAPF-EVFLYKKNKMIQT-LTNKSKIQ--NVGTYELHVGDTID-----LIFNSEHQ 106
DB 175 VVPIASLNPYOSKMTVRAVTKGQIRFTWSNSRGSKLFSIEMVDSGEIRATAFNEQAD 234
QY 107 -----VLKNNTYV--GIILLNPOFIS 126
DB 235 KFFSIIEVKNXYFSGKGTLLKIANKQYTS 262

RESULT 14
PCT-US93-02475-2
; Sequence 2, Application PC/TUS9302475
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Bernadine J.
; TITLE OF INVENTION: Tumor Necrosis Factor with Modified
; TITLE OF INVENTION: Ion Channel
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Donald G. Lewis
; STREET: 8328 Regents Road #1E
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage
; COMPUTER: VE System 386
; OPERATING SYSTEM: MS-DOS 5
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02475
; FILING DATE: 19930412
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,625
; FILING DATE: 12 March 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Donald G. Lewis
; REGISTRATION NUMBER: 28636
; REFERENCE/DOCKET NUMBER: BUW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2421
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 157 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Tumor Necrosis Factor (porcine)
OTHER INFORMATION: A blank residue designated by
OTHER INFORMATION: "xaa" is inserted after residue No. 7 of porcine
OTHER INFORMATION: TNF and the sequence numbering is augmented by 1
OTHER INFORMATION: starting with residue No. 8 in order to maximize
PUBLICATION INFORMATION:
AUTHORS: Pauli, U., Beutler, B., and Peterhans, S.
TITLE: Porcine Tumor Necrosis Factor--Cloning with
TITLE: the Polymerase Chain Reaction and Determination of
JOURNAL: Gene
VOLUME: 81
PAGES: 185-191
DATE: 1989
RELEVANT RESIDUES IN SEQ ID NO: 2: 1-157 (includes
PCT-US93-02475-2
; RELEVANT RESIDUES IN SEQ ID NO: one blank)

Query Match          10.5%; Score 71; DB 5; Length 157;
Best Local Similarity 23.9%; Pred. No. 1;
Matches 33; Conservative 19; Mismatches 44; Indels 42; Gaps 7;

QY 17 KWQASSEPCVN--KVSQWKLEILLNGLYLYIGQV-----APNANY--NDVAPFEVR 65
DB 27 QWOGYANALLANGVKLEKLNQLVPTDGLYLYSQVLFRRGGCGSTVFLTHTISR.LAVS 86
QY 66 LYKXKMDIQLTNKSKION-----VGGTYELHVGDTID-----LIF 101
DB 87 YQTKVNLISAI--KSPCQRETPEGAEKAPWEPYILGQVFOLEKDDRLSALINLPDYIDF 144
QY 102 NSEHQVLKNTYWGIIIL 119
DB 145 AESQGV-----YFGIIL 157

RESULT 15
US-09-710-279-606
; Sequence 606, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 606
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-606

Query Match          10.5%; Score 71; DB 4; Length 620;
Best Local Similarity 23.0%; Pred. No. 7.8;
Matches 26; Conservative 20; Mismatches 33; Indels 34; Gaps 4;

QY 16 SKWQASSEPCVKNKVDWKLEILLNGLYLYIGQVAPNANYDVAPFEVRLYKKNKMDIQT 75
DB 450 NEWORI-----MMSQGRFVVLANGVEVLYGYTTINVD-----DVTVGINRPIYQN 495
QY 76 L-----TNKSKIONVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILANPQ 123
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Tue Nov 2 13:51:41 2004

us-10-080-455-1_copy_52_177.raii

Page 7

Db 496 YHPFEGFNKSRKRN-----LFSIEHRLNKGNTTFPIYAAGVQ 533

Search completed: November 2, 2004, 13:00:14
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:58:53 ; Search time 126 Seconds
(without alignments)
324.216 Million cell updates/sec

Title: US-10-080-455-1_COPY_52_177

Perfect score: 675

Sequence: 1 ETKKEPCMAKFGPLPSKWMQM.....VLKNNTYWGIIILANPQFIS 126

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications_AA:*
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20: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	675	100.0	169	9 US-09-345-790-2	Sequence 2, Appl1
2	675	100.0	169	13 US-10-136-511-2	Sequence 1, Appl1
3	675	100.0	177	13 US-10-080-455-1	Sequence 16, Appl1
4	675	100.0	177	13 US-10-116-378-16	Sequence 39, Appl1
5	675	100.0	177	14 US-10-151-882-39	Sequence 40, Appl1
6	675	100.0	177	14 US-10-218-547-40	Sequence 44, Appl1
7	675	100.0	177	14 US-10-310-793-44	Sequence 40, Appl1
8	675	100.0	177	15 US-10-202-062-40	Sequence 17, Appl1
9	608	90.1	113	14 US-10-338-083-17	Sequence 17, Appl1
10	608	90.1	113	16 US-10-611-399-17	Sequence 12610, A
11	75.5	11.2	5795	9 US-09-815-242-12610	Sequence 2, Appl1
12	74	11.0	543	9 US-09-757-041-2	Sequence 35, Appl1
13	74	11.0	543	14 US-10-004-378A-35	

14	74	11.0	566	8 US-08-813-323A-1	Sequence 1, Appl1
15	74	11.0	567	14 US-10-242-212-7	Sequence 7, Appl1
16	74	11.0	567	14 US-10-207-655-103	Sequence 103, App
17	74	11.0	568	8 US-08-813-323A-2	Sequence 2, Appl1
18	74	11.0	568	14 US-10-116-275-173	Sequence 173, App
19	74	11.0	568	14 US-10-004-378A-36	Sequence 36, Appl1
20	74	11.0	568	15 US-10-042-865-166	Sequence 166, App
21	74	11.0	819	16 US-10-437-963-184313	Sequence 184313,
22	73.5	10.9	1419	16 US-10-437-963-125464	Sequence 125464,
23	73	10.8	313	15 US-10-424-599-231929	Sequence 231929,
24	73	10.8	514	14 US-10-295-074-49	Sequence 49, Appl1
25	73	10.8	514	14 US-10-295-074-51	Sequence 51, Appl1
26	73	10.8	514	14 US-10-295-074-59	Sequence 59, Appl1
27	73	10.8	517	15 US-10-295-074-53	Sequence 53, Appl1
28	72	10.7	601	15 US-10-424-599-209463	Sequence 209463,
29	72	10.7	609	14 US-10-372-686-6	Sequence 6, Appl1
30	72	10.7	609	14 US-10-371-558-6	Sequence 6, Appl1
31	72	10.7	609	14 US-10-375-553-6	Sequence 6, Appl1
32	72	10.7	609	15 US-10-372-553-6	Sequence 6, Appl1
33	72	10.7	624	16 US-10-437-963-153543	Sequence 153543,
34	71.5	10.6	252	14 US-10-154-759-16	Sequence 16, Appl1
35	71.5	10.6	252	14 US-10-154-759-18	Sequence 18, Appl1
36	71.5	10.6	260	14 US-10-154-759-17	Sequence 17, Appl1
37	71.5	10.6	260	14 US-10-154-759-15	Sequence 15, Appl1
38	71.5	10.6	377	14 US-10-295-027-280	Sequence 280, App
39	71	10.5	157	14 US-10-295-074-42	Sequence 42, Appl1
40	71	10.5	290	15 US-10-282-122A-71355	Sequence 71355, A
41	71	10.5	685	9 US-09-815-242-13477	Sequence 13477, A
42	71	10.5	685	15 US-10-282-122A-74118	Sequence 74118, A
43	71	10.5	685	16 US-10-474-776-710	Sequence 710, App
44	70.5	10.4	724	16 US-10-437-963-159310	Sequence 159310,
45	70	10.4	158	14 US-10-297-942-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-345-790-2
; Sequence 2, Application US/09345790
; Patent No. US2002009198A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jjian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,790
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,227
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 169 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-345-790-2

Query Match 100.0%; Score 675; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 3,1e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDA 60
DB 44 ETAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDA 103
QY 61 PPEVRLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 120
DB 104 PPEVRLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 163
QY 121 NPQFIS 126
DB 164 NPQFIS 169

RESULT 2

US-10-136-511-2
; Sequence 2, Application US/10136511
; Publication No. US20020168729A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
; FILE REFERENCE: 1468.0470007/EKS/PSC
; CURRENT APPLICATION NUMBER: US/10/136,511
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/513,584
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/345,790
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/136,788
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/122,099
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 08/912,227
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: 60/024,058
; PRIOR FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-136-511-2

Query Match 100.0%; Score 675; DB 13; Length 169;
Best Local Similarity 100.0%; Pred. No. 3,1e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDA 60
DB 44 ETAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDA 103
QY 61 PPEVRLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 120
DB 104 PPEVRLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 163
QY 121 NPQFIS 126
DB 164 NPQFIS 169

RESULT 3

US-10-080-455-1
; Sequence 1, Application US/10080455
; Publication No. US20020146389A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Masters, Scott A.
; APPLICANT: Pitti, Robert M.
; TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
; FILE REFERENCE: P1150R2
; CURRENT APPLICATION NUMBER: US/10/080,455
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/195,368
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: US 60/069,661
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/065,635
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-455-1

Query Match 100.0%; Score 675; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 3,3e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDA 60
DB 52 ETAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDA 111
QY 61 PPEVRLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 120
DB 112 PPEVRLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 171
QY 121 NPQFIS 126
DB 172 NPQFIS 177

RESULT 4

US-10-116-378-16
; Sequence 16, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Masters, Scott A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 16
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-116-378-16

Query Match 100.0%; Score 675; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCMAKFGPLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANYNDVA 60
52 EIAKEPCMAKFGPLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANYNDVA 111
DB 61 PFEVRLYKXNDMTQTLTKNSKIQNVGGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILLA 120
112 PFEVRLYKXNDMTQTLTKNSKIQNVGGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILLA 171

QY 121 NPOFIS 126
172 NPOFIS 177

RESULT 5

US-10-151-882-39
Sequence 39, Application US/10151882
Publication No. US20030059862A1

GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
FILE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
PRIORITY REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
PRIOR FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 39
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-10-151-882-39

Query Match 100.0%; Score 675; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCMAKFGPLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANYNDVA 60
52 EIAKEPCMAKFGPLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANYNDVA 111
DB 61 PFEVRLYKXNDMTQTLTKNSKIQNVGGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILLA 120
112 PFEVRLYKXNDMTQTLTKNSKIQNVGGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILLA 171
QY 121 NPOFIS 126
172 NPOFIS 177

RESULT 6

US-10-218-547-40
Sequence 40, Application US/10218547
Publication No. US20030100074A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
FILE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
TITLE OF INVENTION: Human Endokline Alpha
FILE REFERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
PRIOR FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/330,761
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.1

SEQ ID NO 40
LENGTH: 177
TYPE: PRT
ORGANISM: human
US-10-218-547-40

Query Match 100.0%; Score 675; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCMAKFGPLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANYNDVA 60
52 EIAKEPCMAKFGPLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANYNDVA 111
DB 61 PFEVRLYKXNDMTQTLTKNSKIQNVGGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILLA 120
112 PFEVRLYKXNDMTQTLTKNSKIQNVGGTYELAHVGDITDILFNSEHQVLYKNTYWGIIILLA 171

QY 121 NPOFIS 126
172 NPOFIS 177

RESULT 7

US-10-310-793-44
Sequence 44, Application US/10310793
Publication No. US20030198640A1

GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A
APPLICANT: Zhang, Jun
APPLICANT: Wei, Bing
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
FILE REFERENCE: PF573
CURRENT APPLICATION NUMBER: US/10/310,793
PRIOR FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 60/336,695
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 10/226,294
PRIOR FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/314,381
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/699,059
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/278,449
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 09/559,290
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/134,067
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/132,227
PRIOR FILING DATE: 1999-05-03
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 177
TYPE: PRT
ORGANISM: human
US-10-310-793-44

Query Match 100.0%; Score 675; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCMAKFGPLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANYNDVA 60

Db 52 ETAKPCKAKGFLPSKQWASSSEPCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVA 111
QY 61 PFEVRLYKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 120
Db 112 PFEVRLYKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 171
QY 121 NPQFIS 126
Db 172 NPQFIS 177

RESULT 8
US-10-202-062-40
; Sequence 40, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 177
; TYPE: PRT
; ORGANISM: human
US-10-202-062-40

Query Match 100.0%; Score 675; DB 15; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPCKAKGFLPSKQWASSSEPCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVA 60
Db 52 ETAKPCKAKGFLPSKQWASSSEPCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVA 111
QY 61 PFEVRLYKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 120
Db 112 PFEVRLYKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 171
QY 121 NPQFIS 126
Db 172 NPQFIS 177

RESULT 9
US-10-338-083-17
; Sequence 17, Application US/10338083
; Publication No. US2003016559A1
; GENERAL INFORMATION:
; APPLICANT: Desjardais, John R.
; APPLICANT: Tansey, Maitu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-17
Query Match 90.1%; Score 608; DB 14; Length 113;

Best Local Similarity 100.0%; Pred. No. 5.7e-60;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CMAKFGPLPSKQWASSSEPCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVAFPEVRL 66
Db 1 CMAKFGPLPSKQWASSSEPCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVAFPEVRL 60
QY 67 YKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 119
Db 61 YKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 113

RESULT 10
US-10-611-399-17
; Sequence 17, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Desjardais, John R.
; APPLICANT: Tansey, Maitu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT APPLICATION NUMBER: US/10/611,399
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-399-17

Query Match 90.1%; Score 608; DB 16; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.7e-60;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CMAKFGPLPSKQWASSSEPCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVAFPEVRL 66
Db 1 CMAKFGPLPSKQWASSSEPCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVAFPEVRL 60
QY 67 YKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 119
Db 61 YKXKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHQLKNNTYGIIILA 113

RESULT 11
US-09-815-242-12610
; Sequence 12610, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant U.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: fastseq for windows version 4.0
SEQ ID NO 12610
LENGTH: 5795
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12610

Query Match 11.2%; Score 75.5; DB 9; Length 5795;
Best Local Similarity 27.4%; Pred. No. 3.5e+02;
Matches 31; Conservative 17; Mismatches 40; Indels 25; Gaps 6;

QY 14 LPSKMQASSEPCVKNVSKLEITLNGLYLYGVAPNANNVDAPEFVRLYKKNKMT 73
DB 952 LPSGWTSLTK-----SDNK-----NGSLAITGRVSNMQAFNSDITTFKV---SATDNV 996
QY 74 QLTNKSXIONVGTVEHYVGDITDLTFNSEHGYLKNNTYWGIIILANPQFIS 126
DB 997 NNTTDSQSKHV-----SIHVK-----ISEDAHPVLGNT--EKVVVNPTAVS 1039

RESULT 12
US-09-757-041-2
Sequence 2, Application US/09757041
Patent No. US20020009726A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: CD40 Associated Proteins
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/757,041
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/349,357
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-757-041-2

Query Match 11.0%; Score 74; DB 9; Length 543;
Best Local Similarity 28.3%; Pred. No. 23;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPCVKNVSKD-----KLEITLNGLYLYGVAPNANN---YNDVAPFVRLYKKN 70
DB 228 ASSAVGHVNLKEMSNLSLEKVSILQV-----ESVERKNSISQSLHNQICSFLEIEROK 261
QY 71 DMIQTLNKSXIONVGTVEHYVGDITDLTFNSEHGYLKN 109
DB 282 EMLR--NNESKI-----LHLQRVLD---SQAEKTK 306

RESULT 13
US-10-004-378A-35
Sequence 35, Application US/10004378A
Publication No. US20030226301A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Furtak, Kazaryna
APPLICANT: Perna, Amanda
APPLICANT: Patunajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Casman, Stacie J
APPLICANT: Burgess, Catherine E
APPLICANT: Malysankar, Uriel M
APPLICANT: Tchernev, Velizar T
APPLICANT: Vermet, Corrine A
APPLICANT: Spytek, Kimberly A
APPLICANT: Agee, Michele
APPLICANT: Rastelli, Luca
APPLICANT: Shenoy, Suresh G
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Gerlach, Valerie
APPLICANT: Edinger, Schlomit
APPLICANT: MacDougall, John R
APPLICANT: Peyman, John A
APPLICANT: Gunther, Erik
APPLICANT: Stone, David J
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esba A
TITLE OF INVENTION: No. US20030226301A1 Human Proteins, Polynucleotides Encoding Th
FILE REFERENCE: 21402-179
CURRENT APPLICATION NUMBER: US/10/004,378A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/242,882
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,765
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/300,206
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/242,789
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,768
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,767
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/243,622
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/273,047
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/243,591
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,950
PRIOR FILING DATE: 2000-10-27
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NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn Ver. 2.1

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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:52:52 ; Search time 461 Seconds
(without alignments)
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Title: US-10-080-455-1_COPY_52_177

Perfect score: 675
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Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	675	100.0	169	1	PCT-US96-13282-2	Sequence 2, Appli
3	675	100.0	169	27	US-10-136-511-2	Sequence 2, Appli
4	675	100.0	177	1	PCT-US01-46625-3	Sequence 3, Appli
5	675	100.0	177	1	PCT-US02-16106-39	Sequence 39, Appli
6	675	100.0	177	1	PCT-US02-23782-40	Sequence 40, Appli
7	675	100.0	177	1	PCT-US02-25809-40	Sequence 40, Appli
8	675	100.0	177	15	US-09-195-368-1	Sequence 1, Appli
9	675	100.0	177	16	US-09-247-225-16	Sequence 16, Appli
10	675	100.0	177	20	US-09-613-972-14	Sequence 14, Appli
11	675	100.0	177	20	US-09-613-972A-14	Sequence 14, Appli
12	675	100.0	177	26	US-10-080-455-1	Sequence 1, Appli
13	675	100.0	177	27	US-10-116-378-16	Sequence 16, Appli
14	675	100.0	177	27	US-10-151-882-39	Sequence 39, Appli
15	675	100.0	177	27	US-10-170-205E-28226	Sequence 28226, A
16	675	100.0	177	28	US-10-202-062-40	Sequence 40, Appli
17	675	100.0	177	28	US-10-218-547-40	Sequence 40, Appli
18	675	100.0	177	29	US-10-310-793-44	Sequence 44, Appli
19	675	100.0	177	30	US-10-405-027-3007	Sequence 3007, Ap
20	675	100.0	177	30	US-10-442-108-5	Sequence 5, Appli
21	675	100.0	177	33	US-10-713-391-1	Sequence 1, Appli
22	675	100.0	177	34	US-10-853-032-9	Sequence 9, Appli
23	608	90.1	113	29	US-10-338-083-17	Sequence 17, Appli
24	608	90.1	113	32	US-10-611-399-17	Sequence 17, Appli
25	566	83.9	508	1	PCT-US01-08631-47785	Sequence 47785, A
26	444	65.8	140	17	US-09-307-140-897	Sequence 897, App
27	444	65.8	140	23	US-09-817-076-897	Sequence 897, App
28	348	51.6	173	34	US-10-853-032-2	Sequence 2, Appli
29	84.5	12.5	1221	30	US-10-417-884-3959	Sequence 3959, Ap
30	84.5	12.5	1221	30	US-10-417-884A-3959	Sequence 3959, Ap
31	78.5	11.7	32	36	US-60-581-351-10793	Sequence 10793, Ap
32	78.5	11.6	599	30	US-10-415-182A-1042	Sequence 1042, Ap
33	77	11.4	183	19	US-09-513-996A-54423	Sequence 54423, A
34	77	11.4	217	32	US-10-603-111-20671	Sequence 20671, A
35	77	11.4	217	36	US-60-096-409-20671	Sequence 20671, A
36	77	11.4	228	19	US-09-513-996A-54422	Sequence 54422, A
37	77	11.4	230	19	US-09-513-996A-54421	Sequence 54421, A
38	77	11.4	851	36	US-60-382-898-362	Sequence 362, App
39	76	11.3	2763	18	US-09-490-190-2	Sequence 2, Appli
40	75.5	11.2	314	22	US-08-791-537-120159	Sequence 120159, A
41	75.5	11.2	3829	12	US-08-827-356-5567	Sequence 5567, Ap
42	75.5	11.2	3829	20	US-09-611-529-4591	Sequence 4591, Ap
43	75.5	11.2	3829	25	US-09-950-084-4591	Sequence 4591, Ap
44	75.5	11.2	5795	1	PCT-US02-03987-12610	Sequence 12610, A
45	75.5	11.2	5795	23	US-09-815-242-12610	Sequence 12610, A

ALIGNMENTS

RESULT 1
PCT-US00-04722-2
; Sequence 2, Application PC/TUS0004722
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: NI, Jian
; TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US00/04722
FILING DATE: 25-FEB-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/122,099
FILING DATE: 26-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/136,788
FILING DATE: 28-MAY-1999
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.047PC06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US00-04722-2

Query Match      100.0%; Score 675; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.3e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKEPCAKRGPLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 60
DB 44 ETAKEPCAKRGPLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKDKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB 104 PFEVRLYNKDKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
QY 121 NPQFIS 126
DB 164 NPQFIS 169

RESULT 2
PCT-US96-13282-2
Sequence 2, Application PC/TUS9613282
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: 9410 Key West Avenue
APPLICANT: Rockville, MD 20850
APPLICANT: United States of America
APPLICANT: APPLICANTS/INVENTORS: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13282
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.047PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13282-2

Query Match      100.0%; Score 675; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.3e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKEPCAKRGPLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 60
DB 44 ETAKEPCAKRGPLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKDKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB 104 PFEVRLYNKDKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
QY 121 NPQFIS 126
DB 164 NPQFIS 169

RESULT 3
US-10-136-511-2
Sequence 2, Application US/10136511
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
FILE REFERENCE: 1488.0470007/EKS/PSC
CURRENT APPLICATION NUMBER: US/10/136,511
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/513,584
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/345,790
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/136,788
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/122,099
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 08/912,227
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: 60/024,058
PRIOR FILING DATE: 1996-08-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 169
TYPE: PRT
ORGANISM: Homo sapiens
US-10-136-511-2

Query Match      100.0%; Score 675; DB 27; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.3e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKEPCAKRGPLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 60
DB 44 ETAKEPCAKRGPLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKDKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB 104 PFEVRLYNKDKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
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QY 121 NPOFIS 126
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Db 164 NPOFIS 169

RESULT 4
PCT-US01-46625-3

; Sequence 3, Application PC/TUS0146625
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C
; APPLICANT: Bieglecki, Karyn M
; APPLICANT: Sun, Xiao
; TITLE OF INVENTION: HAPLOTYPES OF THE TNFSF18 GENE
; FILE REFERENCE: TNFSF18.MMH-1787PCT
; CURRENT APPLICATION NUMBER: PCT/US01/46625
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/247,501
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-46625-3

Query Match 100.0%; Score 675; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 8.8e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 60
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Db 52 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 111
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QY 61 PFEVRLYKXKMDIQTITNKSQIONVGTYELHVGDTIDLLFENSEHOVLKNNYWGIIILLA 120
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Db 112 PFEVRLYKXKMDIQTITNKSQIONVGTYELHVGDTIDLLFENSEHOVLKNNYWGIIILLA 171
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QY 121 NPOFIS 126
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Db 172 NPOFIS 177

RESULT 5
PCT-US02-16106-39

; Sequence 39, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PFS54PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16106-39

Query Match 100.0%; Score 675; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 8.8e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 60
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Db 52 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 111
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QY 61 PFEVRLYKXKMDIQTITNKSQIONVGTYELHVGDTIDLLFENSEHOVLKNNYWGIIILLA 120
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Db 112 PFEVRLYKXKMDIQTITNKSQIONVGTYELHVGDTIDLLFENSEHOVLKNNYWGIIILLA 171
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QY 121 NPOFIS 126
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Db 172 NPOFIS 177

RESULT 6
PCT-US02-23782-40

; Sequence 40, Application PC/TUS0223782
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PFS59PCT
; CURRENT APPLICATION NUMBER: PCT/US02/23782
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 177
; TYPE: PRT
; ORGANISM: human
PCT-US02-23782-40

Query Match 100.0%; Score 675; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 8.8e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 60
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Db 52 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 111
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QY 61 PFEVRLYKXKMDIQTITNKSQIONVGTYELHVGDTIDLLFENSEHOVLKNNYWGIIILLA 120
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Db 112 PFEVRLYKXKMDIQTITNKSQIONVGTYELHVGDTIDLLFENSEHOVLKNNYWGIIILLA 171
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QY 121 NPOFIS 126
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Db 172 NPOFIS 177

RESULT 7
PCT-US02-25809-40

; Sequence 40, Application PC/TUS0225809
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; FILE REFERENCE: PFS61PCT
; CURRENT APPLICATION NUMBER: PCT/US02/25809
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 177
; TYPE: PRT
; ORGANISM: human
PCT-US02-25809-40

Query Match 100.0%; Score 675; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 8.8e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 60
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Db 52 ETKPECMKAFGLPSKQWASSEPPCVNKVSDMKLEILLQNGLYLYIGVAPNANYNDVA 111
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QY	61	PEFVRIRYKKKMDIQTITNSKSIQNGVGYEALHVGSTIDILINSEHQVALKNNITWGIILLA	120
Db	112	PEFVRIRYKKKMDIQTITNSKSIQNGVGYELAHVGSTIDILINSEHQVALKNNITWGIILLA	171
QY	121	NPQGIS	126
Db	172	NPQGIS	177

RESULT 8
US-09-195-368-1
; Sequence 1, Application US/09195368A

```

1 GENERAL INFORMATION:
2 APPLICANT: Ashkenazi, Avi J.
3 APPLICANT: Baker, Kevin P.
4 APPLICANT: Godowski, Paul J.
5 APPLICANT: Gurney, Austin L.
6 APPLICANT: Mark, Melanie R.
7 APPLICANT: Masters, Scott A.
8 APPLICANT: Pitti, Robert M.
9 TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
10 FILE REFERENCE: P115082
11 CURRENT APPLICATION NUMBER: US/09/195,368A
12 CURRENT FILING DATE: 1998-11-18
13 EARLIER APPLICATION NUMBER: US 60/069,661
14 EARLIER FILING DATE: 1997-12-12
15 EARLIER APPLICATION NUMBER: US 60/065,635
16 EARLIER FILING DATE: 1997-11-18
17 NUMBER OF SEQ ID NOS: 8
18 SEQ ID NO 1
19 LENGTH: 177
20 TYPE: ERT
21 ORGANISM: Homo sapiens
22 JS-09-195-368-1

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Query Match	100.0%;	Score 675;	DB 15;	Length 177;
Best Local Similarity	100.0%;	Pred. No. 8.8e-71;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ETAKCECMKAFGFLPEKQWMASSPEPCVAKVSDWLTLETLQNGFLYILIGQVAPNANYNDA 60

Db 52 ETAKCECMKAFGFLPEKQWMASSPEPCVAKVSDWLTLETLQNGFLYILIGQVAPNANYNDA 111

QY 61 PEVPRVLYKKNDMTQTLTNKSKLONIGMYELHVGSDTLINSEHOYKKNNTWGIILLA 120

Db 112 PEVPRVLYKKNDMTQTLTNKSKLQNGGYIELHVGSDTLINSEHOYKKNNTWGIILLA 171

QY 121 NPQFIS 126

Db 172 NPQFIS 177

RESULT 9
US-09-247-225-16
; Sequence 16, Application US/09247225A

```

1 GENERAL INFORMATION:
2 APPLICANT: Ashkenazi, Avi J.
3 APPLICANT: Goddard, Audrey
4 APPLICANT: Gurney, Austin
5 APPLICANT: Masters, Scot A.
6 APPLICANT: Pittl, Robert M.
7 APPLICANT: Wood, William
8 TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
9 TITLE OF INVENTION: ACIDS ENCODING THE SAME
10 FILE REFERENCE: P1206R1
11 CURRENT APPLICATION NUMBER: US/09/247,225A
12 CURRENT FILING DATE: 1999-02-09
13 EARLIER APPLICATION NUMBER: US 60/074,087
14 EARLIER FILING DATE: 1998-02-09
15 NUMBER OF SEQ ID NOS: 31
16 SEQ ID NO 16
17 LENGTH: 177

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-247-225-16

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Query Match	100.0%;	Score 675;	DB 16;	Length 177;
Best Local Similarity	100.0%;	Pred. No. 8.8e-71;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ETAKEPCMAKFPDLPSKQWMASSBPPCYNKASDWMLELITQNGLTLITGOVAPNANNYDVA	60
Db	52	ETAKEPCMAKFPGLPSKQWMASSBPPCYNKASDWMLELITQNGLTLITGOVAPNANNYDVA	111
QY	61	PEFVRLYRKXKMDIOTLTNKSKITQNGYGYELHVGDTIDLINSEHOYLKNNYTWIGIILLA	120
Db	112	PEFVRLYRKXKMDIOTLTNKSKITQNGYGYELHVGDTIDLINSEHOYLKNNYTWIGIILLA	171
QY	121	NPOFIS 126	
Db	172	NPOFIS 177	

RESULT 10
US-09-613-972-14
; Sequence 14, Application US/09613972

```

1  APPLICANT: P. Mickey Williams
2  APPLICANT: Mary E. Gerritsen
3  TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND
4  TITLE OF INVENTION: CARDIOVASCULARIZATION BY TUMOR NECROSIS FACTOR
5  TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
6  FILE REFERENCE: P1765R1
7  CURRENT APPLICATION NUMBER: US/09/613,972
8  CURRENT FILING DATE: 2000-07-11
9  PRIOR APPLICATION NUMBER: US 60/143,304
10 PRIOR FILING DATE: 1999-07-12
11 NUMBER OF SEQ ID NOS: 22
12 SEQ ID NO 14
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Query Match	100.0%;	Score 675;	DB 20;	Length 177;
Best Local Similarity	100.0%;	Pred. No. 8.8e-71;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	ETAKPECMKAPGELLSKQOMASSPEPCNKYSIDWKEITLQNGKLITIGQVAPNNYNDVA	60
Db	52	ETAKPECMKAPGELLSKQOMASSPEPCNKYSIDWKEITLQNGKLITIGQVAPNNYNDVA	111
Qy	61	PEFVRLRYKXKMDIQTLLNSKSTQNGTGYELHVGDTDLLFNSHQVAKXNTYAGLITLLA	120
Db	112	PEFVRLRYKXKMDIQTLLNSKSTQNGTGYELHVGDTDLLFNSHQVAKXNTYAGLITLLA	171
Qy	121	NPQFIS	126
Db	172	NPQFIS	177

RESULT 11
US-09-613-972A-14
; Sequence 14, Application US/09613972A

1 APPLICANT: P. Mickey Williams
2 APPLICANT: Mary E. Gerritsen
3 TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND
4 TITLE OF INVENTION: CARDIOVASCULARIZATION BY TUMOR NECROSIS FACTOR
5 TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
6 FILE REFERENCE: P176S1
7 CURRENT APPLICATION NUMBER: US/09/613,972A
8 CURRENT FILING DATE: 2000-07-11
9 PRIOR APPLICATION NUMBER: US 60/143,304
10 PRIOR FILING DATE: 1999-07-12

```

; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-613-972A-14

```

Query Match	100.0%	Score 675; DB 20	Length 177;
Best Local Similarity	100.0%	Pred. Nc.8.8e-71;	
Matches 126; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

QY	Db
1	ETAKEPCMAKFGFLPESKQWMASSPEPCVAKVSDMKLITLQNGVLYITIGQVAPNNAYDVA
52	ETAKEPCMAKFGFLPESKQWMASSPEPCVAKVSDMKLITLQNGVLYITIGQVAPNNAYDVA
61	PEFVRLYKRNKMDIQLTINSKTIQNGGTYELHVGTDILFNSHQVLYKNTTYGILLTA
112	PEFVRLYKRNKMDIQLTINSKTIQNGGTYELHVGTDILFNSHQVLYKNTTYGILLTA

QY	121	NPQFIS	126
Db	172	NPQFIS	177

RESULT 12
US-10-080-455-1
; Sequence 1, Application US/10080455

```

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
; FILE REFERENCE: P115082
; CURRENT APPLICATION NUMBER: US/10/080,455
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/195,368
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: US 60/069,661
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/065,635
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
; OS-10-080-455-1

```

Query Match	100.0%	Score 675;	DB 26;	Length 177;
Best Local Similarity	100.0%;	Pred. No. 8.8e-71;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	ETAKEPOMAKFGLPEKPMOMASSEPPCCVAKVSDMTKEIIONGLYIIYIQVAPENANNYDVA	60
Db	ETAKEPOMAKFGLPEKPMOMASSEPPCCVAKVSDMTKEIIONGLYIIYIQVAPENANNYDVA	111
QY	PEEVRIYKXKNDMIQTITNSKTIQNNGGYIELAVGTTDLINSEHQVAKNTTYGIIILLA	120
Db	PEEVRIYKXKNDMIQTITNSKTIQNNGGYIELAVGTTDLINSEHQVAKNTTYGIIILLA	171

QY	121	NPQFIS	126
Db	172	NPQFIS	177

RESULT 13
US-10-116-378-16
; Sequence 16, Application US/10116378
; GENERAL INFORMATION:

```

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Martlers, Scot A.
APPLICANT: Pittl, Robert M.
APPLICANT: Wood, William
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGY
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/116,378
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 16
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-378-16

Query Match      100.0%;   Score 675;   DB 27;   Length 177;
Best Local Similarity 100.0%;   Pred. No. 8,8e-71;
Matches 126;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```

QY	1	ETAKEPCMAFEGLPESPMQASSEPCVNKVSJWKETIILNQGLYILIGQVAPNANYNDVA	60	
Db	52	ETAKEPCMAFEGLPESPMQASSEPCVNKVSJWKETIILNQGLYILIGQVAPNANYNDVA	111	
QY		61	PEPEALTKNDMLQTLTNKSKIONGGTVELHAGDTDLFNSBHQVLKXNTYGIILLA	120
Db		112	PEPEALTKNDMLQTLTNKSKIONGGTVELHAGDTDLFNSBHQVLKXNTYGIILLA	171
QY		121	NPOFIS 126	
Db		172	NPOFIS 177	

RESULT 14
US-10-151-882-39

```

; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Agai

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1  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (ABRIL)
2
3  FILE REFERENCE: PP554
4
5  CURRENT APPLICATION NUMBER: US/10/151,882
6
7  CURRENT FILING DATE: 2002-05-22
8
9  PRIOR APPLICATION NUMBER: 60/293,100
10
11 PRIOR FILING DATE: 2001-05-24
12
13 NUMBER OF SEQ ID NOS: 48
14
15 SOFTWARE: PatentIn version 3.0

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-39

```

Query March	100.0%	Score 675;	DB 27;	Length 177;
Best Local Similarity	100.0%	Pred. No. 8.8e-71;		
Matches 126; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ETAKEPCMAK
Db	52	ETAKEPCMAK

Qy 61 PEVRRLKKNKMDIOTLNKSKIQNVGGVYELHVGDTDLINSESHQVLKNNYWGIIILIA 120

Db 112 PEVRRLKKNKMDIOTLNKSKIQNVGGVYELHVGDTDLINSESHQVLKNNYWGIIILIA 171

QY 121 NPOFIS 126
| | | | |

Db 1772 NPQETS 1777

```

RESULT 15
US-10-170-205E-28226
; Sequence 28226, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CLO01381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28226
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-28226

```

Query Match	100.0%;	Score 675;	DB 27;	Length 177;
Best Local Similarity	100.0%;	Pred. No. 8.8e-71;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ETAKECCKMAKEGJLPEKXWMASSBEPCKVAKSVDMLTELIONGLPLITIGOVA	PANINAYDVA	60
Db	52	ETAKECCKMAKEGJLPEKXWMASSBEPCKVAKSVDMLTELIONGLPLITIGOVA	PANINAYDVA	111
QY	61	PEKVRILYKXKMDIQTILNKSKITONNGGYELHVGSDTLINSEHOVAKONTWGIITLA	120	
Db	112	PEKVRILYKXKMDIQTILNKSKITONNGGYELHVGSDTLINSEHOVAKONTWGIITLA	171	
QY	121	NPOQFIS	126	
Db	172	NPOQFIS	177	

Search completed: November 2, 2004, 13:08:00
Job time : 462 secs


```
APPLICANT: Thomson, Adam Read
TITLE OF INVENTION: BAF VARIANTS AND METHODS THEREOF
FILE REFERENCE: A-72175-1
CURRENT APPLICATION NUMBER: US/10/794,751
PRIOR FILING DATE: 2004-03-05
PRIOR APPLICATION NUMBER: US 10/338,083
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US 60/452,707
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US 60/482,081
PRIOR FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US 60/523,880
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: US 60/528,104
PRIOR FILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-10-794-751-17
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Query Match          90.1%; Score 608; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 3e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 CMAKGPISKQWASSPPCVNKSVDKLEILONGILYIGVAPNANNYDVAPEFVRL 66
DB 1 CMAKGPISKQWASSPPCVNKSVDKLEILONGILYIGVAPNANNYDVAPEFVRL 60
QY 67 YKNDMIQTLLNKSKIQNVGTYELHVGDTIDLFNSHQVLKNTYWGIIIL 119
DB 61 YKNDMIQTLLNKSKIQNVGTYELHVGDTIDLFNSHQVLKNTYWGIIIL 113
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RESULT 3

```
US-10-220-366A-15820
Sequence 15820, Application US/10220366A
GENERAL INFORMATION:
APPLICANT: HYSBQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: Custom
SEQ ID NO 15820
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(137)
OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-15820
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Query Match          10.4%; Score 70.5; DB 6; Length 137;
Best Local Similarity 30.0%; Pred. No. 0.25;
Matches 30; Conservative 13; Mismatches 38; Indels 19; Gaps 5;
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QY 36 LEILONGILYIGVAPNANNYDVAPEFVRLKNDMIQTLLNKSKIQNVGTYELH-V 93
DB 47 LSIQVG---VHRGIAAMTFALVTP-----NIDRLQELVNRGNSQYRGAKYIIRDN 97
QY 94 GDTIDLFNSHQVLKNTYW-----GIIILANPOFI 125
DB 98 GDRIDLRHPRGSDLHLQTYGVKVRHMCDDGDIVIFNRQCI 137
```

RESULT 4

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US-10-952-698-181
Sequence 181, Application US/10952698
GENERAL INFORMATION:
APPLICANT: Mack, David
APPLICANT: Aziz, Natasha
TITLE OF INVENTION: METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/952,698
CURRENT FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn version 3.2
SEQ ID NO 181
LENGTH: 840
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-952-698-181
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Query Match          10.1%; Score 68; DB 6; Length 840;
Best Local Similarity 18.2%; Pred. No. 5.2;
Matches 24; Conservative 31; Mismatches 35; Indels 42; Gaps 5;
```

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QY 7 CMAKGPISKQWASSPPCVNKSVDKLEILONGILYI-----GVAPNANNYD 58
DB 48 CEAGIKKWSISVPSRP-----FQSLNGLTMTHTNDSGLTNAISHLGRNN 99
QY 59 VAPEFVRLKNDMIQTLLNKSKIQNVGTYELHVGDTIDLFNSHQVLKNTYWG-I-- 116
DB 100 IADIEIGAFNGLGLK-----QLHIN-----HNSLEILKEDFPHGEN 137
QY 117 --IILANPOFIS 126
DB 138 LEFLQADNNFIY 149
```

RESULT 5

```
US-10-948-576-145
Sequence 145, Application US/10948576
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant IL-3 Hematopoietic Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSER: Carol M. Nielsen, Winstead Sechrest & Minick P.C.
STREET: P.O. Box 50784
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75201
COMPUTER READABLE FORM:
MEDIUM TYPE: CD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/948,576
FILING DATE: 22-Sep-2004
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/083,446
```

FILED DATE: 22-FEB-2002
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carol M. Nielsen
REGISTRATION NUMBER: 37,676
REFERENCE/DOCKET NUMBER: 2790/7 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-650-2722
TELEFAX: 214-745-5390
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-10-948-576-145

Query Match 10.0%; Score 67.5; DB 6; Length 317;
Best Local Similarity 28.0%; Pred. No. 1.6;
Matches 28; Conservative 12; Mismatches 27; Indels 33; Gaps 6;

QY 5 EPMAKFGPLPSKQWASPEPCVNVKVS-----LETLONGLYITGVAP 52
DB 70 QPC-----LPSSA-TAPASHPIIIVAGDWQEFREKLTFLVTLTQAOEQYVIEGRISP 122

QY 53 -----NANVNDVAPFEVRLYKNKMI-----OTLTNKSRI 82
DB 123 GGGGGGSGNMAPVPGSE-----DSKDVAAAPHPRLTSSERI 158

RESULT 6
US-10-955-952-24

Sequence 24, Application US/10955952
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C12
CURRENT APPLICATION NUMBER: US/10/955,952
CURRENT FILING DATE: 2004-09-29
PRIOR APPLICATION NUMBER: US/10/121,058
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 24
LENGTH: 285
TYPE: PRT
ORGANISM: Homo Sapien
US-10-955-952-24

Query Match 9.9%; Score 67; DB 6; Length 285;
Best Local Similarity 22.2%; Pred. No. 1.6;
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPECMKFGPLPSKQWASPEPCVNVKVS-----DW-----KLEILQN 41
DB 140 ETVTQDCLQ-----LIADSEFTTQKSGSYTFVFWPLSPKRGSALEKENKILVKEK 190
QY 42 GLYLYIGGVAPNANVNDVAPFEVRLYKNK-----DMIGTLTNKSKIONV----- 85
DB 191 GTFPIYGVVL-----YTDKTYAMGHLIQRKVVHFGDELVLVTLFRCTIQMPPETLPNNSCY 246

QY 86 -GGTYLHVGDITDILFENSEHVLK-----NNTYWGILL 119
DB 247 SAGIAKLBEGDELQLAIPRENNQISLDGVTFFGALKL 284

RESULT 7
US-10-157-779-24

Sequence 24, Application US/10157779
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C426
CURRENT APPLICATION NUMBER: US/10/157,779
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17

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;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See file wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 24
;; LENGTH: 285
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-157-779-24

Query Match
Best Local Similarity 22.2%; Pred. No. 1.6;
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPCKAKGFLPSKQWASSPPCVNKVS---DW-----KLEIIQN 41
Db 140 ETVTQDCIQ-----LADSETPTIQKSYTFVFWLSPKGSALKEKENKILVET 190
QY 42 GLVLIYQVAPNANYNDVAPPEVRLYNNK-----DMIQTLTNKSKIQNV----- 85
Db 191 GYFFIYQVL---YTDKTYAMGHILQKQKHYVFGDELSTVTLFRCIQNMPEITLPNNSCY 246
QY 86 -GGTYELHVGDTIDLIENSEHOVLK--NNTYWGIIIL 119
Db 247 SAGIAKLEEGDELQALPREENAQISLDGDVTFFGALKI 284

RESULT 8
US-10-964-241-24
; Sequence 24, Application US/10964241
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C33
; CURRENT APPLICATION NUMBER: US/10/964,241
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PRIORT APPLICATION NUMBER: US/10/123,236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
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;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See file wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 24
;; LENGTH: 285
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-964-241-24

Query Match
Best Local Similarity 22.2%; Pred. No. 1.6;
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPCKAKGFLPSKQWASSPPCVNKVS---DW-----KLEIIQN 41
Db 140 ETVTQDCIQ-----LADSETPTIQKSYTFVFWLSPKGSALKEKENKILVET 190
QY 42 GLVLIYQVAPNANYNDVAPPEVRLYNNK-----DMIQTLTNKSKIQNV----- 85
Db 191 GYFFIYQVL---YTDKTYAMGHILQKQKHYVFGDELSTVTLFRCIQNMPEITLPNNSCY 246
QY 86 -GGTYELHVGDTIDLIENSEHOVLK--NNTYWGIIIL 119
Db 247 SAGIAKLEEGDELQALPREENAQISLDGDVTFFGALKI 284

RESULT 9
US-10-626-914-9
; Sequence 9, Application US/10626914
; GENERAL INFORMATION:
; Applicant: Chuntharapai, Annan
; Applicant: Docket Preview
; Applicant: GREWAL, IOBAL
; Applicant: KIM, KYUNG JIN
; Applicant: YAN, MINHONG
; TITLE OF INVENTION: TACT Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-9

Query Match
Best Local Similarity 22.2%; Pred. No. 1.6;
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPCKAKGFLPSKQWASSPPCVNKVS---DW-----KLEIIQN 41
Db 140 ETVTQDCIQ-----LADSETPTIQKSYTFVFWLSPKGSALKEKENKILVET 190
QY 42 GLVLIYQVAPNANYNDVAPPEVRLYNNK-----DMIQTLTNKSKIQNV----- 85
Db 191 GYFFIYQVL---YTDKTYAMGHILQKQKHYVFGDELSTVTLFRCIQNMPEITLPNNSCY 246
QY 86 -GGTYELHVGDTIDLIENSEHOVLK--NNTYWGIIIL 119
Db 247 SAGIAKLEEGDELQALPREENAQISLDGDVTFFGALKI 284

RESULT 10
US-10-076-157A-11
; Sequence 11, Application US/10076157A
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/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Seubberger, Harald
/ APPLICANT: Hoeffken, Hans Wolfgang
/ APPLICANT: Doval, Jose Luis Revuelta
/ APPLICANT: Jimenez, Alberto
/ APPLICANT: Garcia, Maria Angeles Santos
/ TITLE OF INVENTION: Phosphoriboxyl-Pyrophosphate Synthetase Polypeptide
/ FILE REFERENCE: PP46687-2/DP
/ CURRENT APPLICATION NUMBER: US/10/076,157A
/ PRIOR FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: Germany, 1975775.5
/ PRIOR FILING DATE: 1997-12-23
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: WordPerfect 8
/ SEQ ID NO 11
/ LENGTH: 525
/ TYPE: PRT
/ ORGANISM: Asibhya gossypii
/ US-10-076-157A-11
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Query Match          9.9%; Score 66.5; DB 6; Length 525;
Best Local Similarity 27.4%; Pred. No. 4.1;
Matches 29; Conservative 16; Mismatches 32; Indels 29; Gaps 7;
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QY 26 PCVAKUSD--WKLE--ILQNGLYLYIGQVAPNANNDVAPFEVRL-----YKXKDMICT 75
DB 42 PCTQKISELQMKKGVILSGPYSVVAADPHV---DRANFELGVPLIGTCYGLQELANI 98
QY 76 LNKSKIQNVG-----GTYELHVGDTIDLINSEHOVLKNNYGIIL 114
DB 99 AG-----AEYGRGEKREYGRATLHVEDSACPLFNN-----VDSSTW 135
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RESULT 11
/ Sequence 15, Application US/10668178
/ GENERAL INFORMATION:
/ APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
/ APPLICANT: MAYUMI, Tadanoiri
/ APPLICANT: TSUTSUMI, Yasuo
/ APPLICANT: NAKAGAWA, Shinsaku
/ APPLICANT: IKEGAMI, Hakuo
/ TITLE OF INVENTION: Biologically-active conjugate
/ FILE REFERENCE: MAYUMI2A
/ CURRENT APPLICATION NUMBER: US/10/668,178
/ PRIOR FILING DATE: 2003-09-24
/ PRIOR APPLICATION NUMBER: JP 83509/2002
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: JP 185387/2002
/ PRIOR FILING DATE: 2002-06-26
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 15
/ LENGTH: 157
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
/ US-10-668-178-15
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Query Match          9.5%; Score 64; DB 6; Length 157;
Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 26; Conservative 21; Mismatches 38; Indels 36; Gaps 5;
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QY 30 KVSMDKLEILQNGLYLYIGQV-----APNANY---NDVAPFEVRLYKXKDMICTLTNKS 80
DB 42 ELRDNQLVVPSSEGLYLYISQVLSGGGCPSTHVLTHHTISRIVASYQTRVNLISALASPC 101
QY 81 KIQN-----VGYTELHVGDTID-----LINSEHOVLKNNYGIIL 118
DB 102 QRETPGAEALPWYEPIDYIGVGFQLETDRLSAEINRPDYLDPAESGQV-----YFGIIA 156
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QY 119 L 119
DB 157 L 157
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RESULT 12
/ Sequence 16, Application US/10668178
/ GENERAL INFORMATION:
/ APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
/ APPLICANT: MAYUMI, Tadanoiri
/ APPLICANT: TSUTSUMI, Yasuo
/ APPLICANT: NAKAGAWA, Shinsaku
/ APPLICANT: IKEGAMI, Hakuo
/ TITLE OF INVENTION: Biologically-active conjugate
/ FILE REFERENCE: MAYUMI2A
/ CURRENT APPLICATION NUMBER: US/10/668,178
/ PRIOR FILING DATE: 2003-09-24
/ PRIOR APPLICATION NUMBER: JP 83509/2002
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: JP 185387/2002
/ PRIOR FILING DATE: 2002-06-26
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 16
/ LENGTH: 157
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: synthetic (Variant protein of human tumor necrosis factor)
/ US-10-668-178-16
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Query Match          9.5%; Score 64; DB 6; Length 157;
Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 26; Conservative 21; Mismatches 38; Indels 36; Gaps 5;
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QY 30 KVSMDKLEILQNGLYLYIGQV-----APNANY---NDVAPFEVRLYKXKDMICTLTNKS 80
DB 42 ELRDNQLVVPSSEGLYLYISQVLSGGGCPSTHVLTHHTISRIVASYQTRVNLISALASPC 101
QY 81 KIQN-----VGYTELHVGDTID-----LINSEHOVLKNNYGIIL 118
DB 102 QRETPGAEALPWYEPIDYIGVGFQLETDRLSAEINRPDYLDPAESGQV-----YFGIIA 156
QY 119 L 119
DB 157 L 157
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RESULT 13
/ Sequence 122, Application US/10948576
/ GENERAL INFORMATION:
/ APPLICANT: Abrams, Mark A.
/ APPLICANT: Bauer, S. C.
/ APPLICANT: Braford-Goldberg, Sarah R.
/ APPLICANT: Caparon, Mair H.
/ APPLICANT: Easton, Alan M.
/ APPLICANT: Klein, Barbara K.
/ APPLICANT: McKeatn, John P.
/ APPLICANT: Olin, Peter O.
/ APPLICANT: Paik, Kumman
/ APPLICANT: Thomas, John W.
/ TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
/ USING Multivariant IL-3 Hematopoiesis Chimera Proteins
/ NUMBER OF SEQUENCES: 197
/ CORRESPONDENCE ADDRESS:
/ ADDRESSSEE: Carol M. Nielsen, Winstead Sechrest & Minick P.C.
/ STREET: P.O. Box 50784
/ CITY: Dallas
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 75201
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/948,576
FILING DATE: 22-Sep-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/083,446
FILING DATE: 22-FEB-2002
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carol M. Nielsen
REGISTRATION NUMBER: 37,676
REFERENCE/DOCKET NUMBER: 2790/7 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-650-2722
TELEFAX: 214-745-5390
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 122:
US-10-948-576-122

Query Match          9.5%; Score 64; DB 6; Length 307;
Best Local Similarity 25.9%; Pred. No. 3.9;
Matches 29; Conservative 11; Mismatches 40; Indels 32; Gaps 5;

QY 5 EPCMAKGPILPSKQWASSPPCVNKVSDMK-----LEILONGILYLYGVAP 52
DB 70 QPC-----LPSA-TAAPSRRHPIIKAGDWQEFREKLTFLYVLTLEQAQEQYVLEGKISP 122
QY 53 NANYNDVAFPEVRLYKKNKDMIQTLTKNS-----KIQNVG-----GTVEL 91
DB 123 GGSGGSGSNMATPLGPASSLPSQSFILKSLBQVRIQDGAALQKCATYTL 174

RESULT 14
US-10-948-576-123
; Sequence 123, Application US/10948576
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
;           Bauer, S. C.
;           Bradford-Goldberg, Sarah R.
;           Caparon, Maïre H.
;           Easton, Alan M.
;           Klein, Barbara K.
;           McKearn, John P.
;           Oline, Peter O.
;           Paik, Kumnan
;           Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant IL-3 Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol M. Nielsen, Winstead Secrest & Minick P.C.
STREET: P.O. Box 50784
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75201
COMPUTER READABLE FORM:
MEDIUM TYPE: CD
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MEDIUM TYPE: CD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/948,576
FILING DATE: 22-Sep-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/083,446
FILING DATE: 22-FEB-2002
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carol M. Nielsen
REGISTRATION NUMBER: 37,676
REFERENCE/DOCKET NUMBER: 2790/7 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-650-2722
TELEFAX: 214-745-5390
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-10-948-576-123

Query Match          9.5%; Score 64; DB 6; Length 307;
Best Local Similarity 25.9%; Pred. No. 3.9;
Matches 29; Conservative 11; Mismatches 40; Indels 32; Gaps 5;

QY 5 EPCMAKGPILPSKQWASSPPCVNKVSDMK-----LEILONGILYLYGVAP 52
DB 70 QPC-----LPSA-TAAPSRRHPIIKAGDWQEFREKLTFLYVLTLEQAQEQYVLEGKISP 122
QY 53 NANYNDVAFPEVRLYKKNKDMIQTLTKNS-----KIQNVG-----GTVEL 91
DB 123 GGSGGSGSNMATPLGPASSLPSQSFILKSLBQVRIQDGAALQKCATYTL 174

RESULT 15
US-10-948-576-135
; Sequence 135, Application US/10948576
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
;           Bauer, S. C.
;           Bradford-Goldberg, Sarah R.
;           Caparon, Maïre H.
;           Easton, Alan M.
;           Klein, Barbara K.
;           McKearn, John P.
;           Oline, Peter O.
;           Paik, Kumnan
;           Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant IL-3 Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol M. Nielsen, Winstead Secrest & Minick P.C.
STREET: P.O. Box 50784
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75201
COMPUTER READABLE FORM:
MEDIUM TYPE: CD
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1 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
3 SOFTWARE: Patent In Release #1.0, Version #1.25
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5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/10/948,576
7 FILING DATE: 22-Sep-2004
8 CLASSIFICATION: <Unknown>
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10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 10/083,446
12 FILING DATE: 22-FEB-2002
13 APPLICATION NUMBER: 08/762,227
14 FILING DATE: 09-DEC-1996
15 APPLICATION NUMBER: US 08/192,325
16 FILING DATE: 14-FEB-1994
17 APPLICATION NUMBER: US 08/446,872
18 FILING DATE: 06-JUN-1995
19
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Carol M. Nielsen
22 REGISTRATION NUMBER: 37,676
23 REFERENCE/DOCKET NUMBER: 2790/7 US
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 713-650-2722
26 TELEFAX: 214-745-5390
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28 INFORMATION FOR SEQ ID NO: 135:
29 SEQUENCE CHARACTERISTICS:
30     LENGTH: 307 amino acids
31     TYPE: amino acid
32     STRANDEDNESS: <Unknown>
33     TOPOLOGY: linear
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35 MOLECULE TYPE: protein
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39 US-10-948-576-135
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41 Query Match: 9.5%, Score 64, DB 6, Length 307,
42 Best Local Similarity 25.9%, Pred. No. 3.9, IndeIs 32, Gaps 5
43 Matches 29, Conservative 11, Mismatch 40,
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Job time : 13 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:50:22 ; Search time 38 seconds

(without alignments)
319.035 Million cell updates/sec

Title: US-10-080-455-1_COPY_52_177

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	11.4	851	2 T51545	receptor protein k
2	75.5	11.2	314	2 I50811	MHC class I protei
3	75.5	11.2	3890	2 C89921	hypothetical prote
4	75	11.1	575	2 T28230	ORF MSV069 probabl
5	74	11.0	233	2 S11688	tumor necrosis fac
6	74	11.0	543	2 S68467	CD40 receptor-asso
7	74	11.0	567	2 A59272	CD40 receptor-asso
8	74	11.0	568	2 A59600	CD40 receptor-asso
9	73.5	10.9	504	2 T47446	hypothetical prote
10	72	10.7	393	2 D75207	hypothetical prote
11	72	10.7	477	2 S32223	penicillin-binding
12	72	10.7	486	2 E35665	hypothetical prote
13	72	10.7	525	2 E70125	hypothetical prote
14	72	10.7	609	1 A43458	repliation protei
15	71.5	10.6	1123	2 A72311	conserved hypotet
16	71.5	10.6	3623	2 T08618	intrinsic factor-B
17	71	10.5	232	1 S12606	tumor necrosis fac
18	71	10.5	473	2 S39404	penicillin-binding
19	71	10.5	486	2 D55965	penicillin-binding
20	71	10.5	486	2 B35965	penicillin-binding
21	71	10.5	486	2 B35965	penicillin-binding
22	71	10.5	486	2 C35965	penicillin-binding
23	71	10.5	679	2 S06000	penicillin-binding
24	71	10.5	680	2 G95194	penicillin-binding
25	71	10.5	685	2 D98061	penicillin-binding
26	70.5	10.4	297	2 T28188	hypothetical prote
27	70.5	10.4	890	2 A30481	bacteriocin BCNS -
28	70.5	10.4	1508	2 T31098	probable dextran su
29	70	10.4	1010	2 T33372	hypothetical prote

30	69.5	10.3	234	1 A25451	tumor necrosis fac
31	69.5	10.3	351	2 S67649	MSS2 protein - yea
32	69.5	10.3	989	2 A54505	serine-repeat anti
33	69.5	10.3	997	2 B71617	SERA antigen/papal
34	69.5	10.3	1236	2 B35329	hypothetical prote
35	68.5	10.1	129	2 B35216	FP14 protein - fow
36	68.5	10.1	187	2 B72666	hypothetical prote
37	68.5	10.1	290	2 S59322	hypothetical prote
38	68.5	10.1	326	1 VGXR25	glycoprotein VP7 p
39	68.5	10.1	326	1 VGXR35	glycoprotein VP7 p
40	68.5	10.1	686	2 T20898	hypothetical prote
41	68.5	10.1	704	2 T29996	hypothetical prote
42	68.5	10.1	1017	2 PC4035	cell-cycle-depende
43	68	10.1	234	1 JQ1344	tumor necrosis fac
44	68	10.1	345	2 B64565	conserved hypotet
45	68	10.1	345	2 E71858	hypothetical prote

ALIGNMENTS

RESULT 1

T51545
receptor protein kinase-like protein - Arabidopsis thaliana

N/Alternate names: protein F2K13_50

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 18-Aug-2000 #sequence_rev18-Aug-2000 #text_change 16-Aug-2004

C/Accession: T51545

R/Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew

Submitted to the Protein Sequence Database, August 2000

A/Accession: T51545

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1851 <SNT>

A/Cross-references: UNIPROT:Q91FL1; EMBL:AJ391141

A/Experimental source: cultivar Columbia; BAC clone F2K13

C/Genetics:

A/Map position: 5

A/Intons: 23/1; 202/2; 371/1; 428/2; 452/2; 476/2; 531/1; 602/3; 645/1; 667/1; 730/2

A/Note: F2K13_50

C/Superfamily: protein kinase homology

Query Match 11.4%; Score 77; DB 2; Length 851;
Best Local Similarity 28.0%; Pred. No. 19;
Matches 28; Conservative 17; Mismatches 27; Indels 28; Gaps 5;

QY	34	WKLEILONGLYL-----YQVAPNANYNDVAPFEVLYKKKMKIGTLTKSKIQNTGCT	88
DB	88	YTLDTVLQNRMYMKAVFVGYNY--DGYNDYPSFDLYLGPVKWVRVDEGK-----VNGS	139
QY	89	YE--LHV-----GDTIDLFSSEHQVLYKNTY	113
DB	140	VEEITHPSSNSIQICLVKIGNSLPFISALERLRIRNDTY	179

RESULT 2

I50811
MHC class I protein, alpha 1, alpha 2, alpha 3 and transmembrane domains - coelacanth (

C/Species: Latimeria chalumnae (coelacanth)

C/Date: 13-Sep-1996 #sequence_rev13-Sep-1996 #text_change 09-Jul-2004

C/Accession: I50811

R/Betz, U.A.K.; Mayer, W.E.; Klein, J.

Proc. Natl. Acad. Sci. U.S.A. 91, 11065-11069, 1994

A/Title: Major histocompatibility complex class I genes of the coelacanth Latimeria cha

A/Reference number: I50810; MUID:95062206; PMID:7972010

A/Accession: I50811

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-314 <BET>

A/Cross-references: UNIPROT:Q31417; EMBL:U08034; NID:G549857; PIDN:AAA52346.1; PID:G5560

C/Genetics:

A/Gene: Lach-UB-01

A:introns: 91/1; 183/1; 276/1
C:superfamily: class I hisocompatibility antigen; immunoglobulin homology

Query Match 11.2%; Score 75.5; DB 2; Length 314;
Best Local Similarity 34.2%; Pred. No. 8;
Matches 26; Conservative 9; Mismatches 26; Indels 15; Gaps 5;

QY 4 KPCMAKFGPLPSKQMASSEPPCVNKVSDMKLEILLONGI--YLITYGOVAPNANVNDVAP 61
DB 138 KQIRKQKCPVDEAMSYSE-----DMKQCEIE-GLKKYLLYK--ETLERKVP 185
QY 62 FEVRLYKKNKMTQTIT 77
DB 186 -EVRYVDRPDLERLNT 200

RESULT 3

C89921
Hypothetical protein ebhB [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C89921
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89921

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-3890 <KUR>

A:Cross-references: UNIPROT:Q9JUS3; GB:BA000018; PID:g13701233; PTDN:BA842528.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: ebhB

Query Match 11.2%; Score 75.5; DB 2; Length 3890;
Best Local Similarity 27.4%; Pred. No. 1.8e+02;
Matches 31; Conservative 17; Mismatches 40; Indels 25; Gaps 6;

QY 14 LPSPKQMASSEPPCVNKVSDMKLEILLONGIYLYIQVAPNANVNDVAPFEVRLYKKNKMTI 73
DB 952 LPSPGTSNLTX-----SDNK-----NGSLAITGRVSMNQAFNSDITFKV---SATDNV 996
QY 74 QLTETKSKLONGVGYELHVGPTIDLIINSEHOVLKNTYWGIIILANPQFIS 126
DB 997 NNTTNDSSQKHV---SIHVGR---ISEDAHPVILGNT--EKVVVAVNPFAVS 1039

RESULT 4

ORF MSV069 Probable rifampicin resistance (RIF) protein, Helicobacter armigeri entomopoxviri

C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T28230

R:Alonso, C.L.; Twilman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359

A:Accession: T28230

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-575 <AF0>

A:Cross-references: UNIPROT:Q9YK23; EMBL:AF063866; NID:g4049647; PTDN:AAC97814.1; PID:g4

C:Genetics:

A:Note: MSV069

C:Superfamily: variola virus N2L protein

Query Match 11.1%; Score 75; DB 2; Length 575;
Best Local Similarity 23.7%; Pred. No. 19;
Matches 32; Conservative 21; Mismatches 56; Indels 26; Gaps 6;

QY 18 KQMASSEPPCVN-----KVSMDKLEILLONGI--GLYLYIGOV-----APNANVNDVAPFE 63
DB 32 YQFTSSSVYENGGLYLYIKTIDSKLEGGNNFGILLITPEIKGISIRQSFVYKLEEFV 91

QY 64 VRLYKKNKMTQTITLNSKIQ-----NGGYELHVGPTIDLI--FNSHOV-----LKN 111
DB 92 IETDNDSTVNTIIKSGLELFEFNRSGSKISKIIGNNIDLCSPNFGYTADDIIFTSRE 151
QY 112 TYWGIIILANPQFIS 126
DB 152 IYFPLITIPDQFIN 166

RESULT 5

S11688
tumor necrosis factor alpha precursor - cat

C:Species: Felis silvestris catus (domestic cat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S11688

R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990

A:Title: Gene sequence of feline tumor necrosis factor alpha.
A:Reference number: S11688; MUID:91016860; PMID:2216740

A:Accession: S11688

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <MCG>

A:Cross-references: UNIPROT:P19101; EMBL:X54000; NID:g1084; PTDN:CAA37948.1; PID:g295777

C:Genetics:

A:introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F19/20/Binding site: myristate (lys) (covalent) #status predicted

F/81/Binding site: carbonylate (Ser) (covalent) #status predicted

F/145-177/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 24.4%; Pred. No. 7.8;
Matches 30; Conservative 21; Mismatches 32; Indels 40; Gaps 6;

QY 30 KVSMDKLEILLONGIYLYIGOV-----APNANV---NDVAPFEVRLYKKNKMTQTITNS 80
DB 118 ELTDNQLKVPDGLYLYISQVLFYGGGCPSTHYVLLTHAISRAVSQYQKVNLSAI--KS 175
QY 81 KIQN-----VGTYELHVGPTID-----LIINSEHOVLKNTYWGII 116
DB 176 PCORTEPGARAKWYBEPIYIGVQLEKGRSLSTEINLPAVLDPAFSGOV-----YFGI 230
QY 117 ILL 119
DB 231 IAL 233

RESULT 6

S68467
CD40 receptor-associated protein CAP-1 - human

C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: S68467; I53498

R:Sato, T.; Irie, S.; Reed, J.C.
FEBS Lett. 358, 113-118, 1995

A:Title: A novel member of the TRAF family of putative signal transducing proteins binds

A:Reference number: I53498; MUID:95126922; PMID:7530216

A:Accession: S68467

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-543 <SAT>

A:Cross-references: UNIPROT:Q13114; EMBL:L38509; NID:g695357; PTDN:AAA68195.1; PID:g695357

A:Experimental source: tissue-type fetal brain

C:Genetics:

A:Gene: CAP-1

C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology

C:Keywords: homodimer; signal transduction; zinc finger

A:Note: sequence extracted from NCBI backbone (NCBIN:113390, NCBI:113391)
A:Note: parts of the sequence determined by protein sequencing
C:Complex: Replication protein A is a trimer of 70K (A1), 32K (A2), and 14K (A3) chains
C:Function:
A:Description: thought to be the eukaryotic equivalent of prokaryotic single-stranded DNA
A:synthesis
A:Pathway: DNA replication initiation
C:Superfamily: replication protein A1
C:Keywords: DNA replication initiation; single-stranded DNA binding; trimer; zinc finger
P:472-494/Region: zinc finger CCCC motif

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:42:32 ; Search time 192 Seconds
(without alignments)
377.590 Million cell updates/sec

Title: US-10-080-455-1_COPY_52_177

Perfect score: 675
Sequence: 1 ETRXEPCKAKFGPLPSKWM.....VAKNTYMGIIILANPQFIS 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_sprot:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	177	1	TN18 HUMAN
2	675	100.0	177	2	AAH63111
3	675	100.0	177	2	AAH63119
4	348	51.6	173	2	Q80Y62
5	348	51.6	173	2	CAE12166
6	348	51.6	173	2	CAE12167
7	344	51.0	173	2	Q7TNW2
8	342	50.7	173	2	Q7TS55
9	342	50.7	173	2	AAQ55265
10	108.5	16.1	172	1	TNF5_CHICK
11	86.5	12.8	516	1	Q861B8
12	85.5	12.7	270	2	Q896D6
13	83	12.3	599	2	O81AW5
14	83	12.3	3063	2	O8QXN1
15	79.5	11.8	459	2	Q6HWA4
16	78.5	11.7	372	1	PROB_OCEBH
17	78.5	11.6	599	2	O8E0H3
18	78.5	11.6	599	2	O8E648
19	78	11.6	695	2	O7R121
20	78	11.6	10746	2	O6GGX3
21	77	11.4	228	2	Q6FHP9
22	77	11.4	368	2	Q6UAA8
23	77	11.4	368	2	AA128927
24	77	11.4	479	2	Q7RB42
25	77	11.4	646	2	O6MCG4
26	77	11.4	646	2	CA23735
27	77	11.4	813	2	O6IM89
28	77	11.4	851	2	Q91FL1
29	77	11.4	3064	2	O8B388
30	76.5	11.3	418	2	O8RFW2
31	76.5	11.3	739	2	O612G6

32	76	11.3	390	2	O61588	O61588 streptococc
33	76	11.3	3063	2	O8QXN2	O8QXN2 sugarcane m
34	75.5	11.2	270	2	Q72T60	Q72T60 leptospira
35	75.5	11.2	270	2	O8F293	O8F293 leptospira
36	75.5	11.2	270	2	AA569768	AA569768 leptospir
37	75.5	11.2	314	2	Q31417	Q31417 latimeria c
38	75.5	11.2	3890	2	O99U53	O99U53 staphylococ
39	75.5	11.2	3890	2	Q9A5M1	Q9A5M1 staphylococ
40	75	11.1	233	1	TNFA_FELCA	TNFA_FELCA felis silve
41	75	11.1	259	2	O6UD54	O6UD54 uncultured
42	75	11.1	259	2	AA05186	AA05186 uncultured
43	75	11.1	332	2	Q7AW75	Q7AW75 nanorarchaeu
44	75	11.1	332	2	AA39283	AA39283 nanorarchaeu
45	75	11.1	422	2	Q7WZ88	Q7WZ88 shewanella

ALIGNMENTS

RESULT 1

TN18 HUMAN

STANDARD;

PRT; 177 AA.

AC Q9UN62; 095852; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 18 (Glucocorticoid-induced TNF-related ligand) (HGTRR) (Activation-inducible TNF-related ligand) (AIRRL) (UNQ149/PRO175)
 GN Name=TNFSF18; Synonyms=AITRL, GITRL, TL6;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RX MEDLINE=99175482; PubMed=10074428;
 RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
 RT "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR.";
 RL Curr. Biol. 9:215-218(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Gu Q., Hass P.E., Heldens S., Batton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J., Sehagiri R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansu D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [3]
 RP SEQUENCE OF 9-177 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99156876; PubMed=10037686;
 RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Tang I.-K., Kim Y.-J., Xing L., Liu D., Wang S.-X., Kwon B.S.;
 RT "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";
 RL J. Biol. Chem. 274:6056-6061(1999).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF18/AITR/GITR. Important for interactions between activated T lymphocytes and endothelial cells and may modulate T lymphocyte survival in peripheral tissues.
 CC -!- SUBUNIT: Homotrimer (Potential).
 CC

```

CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Expressed at high levels in the small
CC intestine, ovary, testis, kidney and endothelial cells.
CC -1- INDUCTION: Up-regulated after stimulation by lipopolysaccharides.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF125303; AAD22634.1; -
DR EMBL; AY358868; AAO89227.1; -
DR EMBL; AF117713; AAD19695.1; -
DR Genew; HGNC:11932; TNFSF18.
DR MIM; 603898; -
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF-like.
DR InterPro; IPR008983; TNF-like.
DR PROSITE; PS00251; TNF_1; FALSE NEG.
DR PROSITE; PS00049; TNF_2; FALSE NEG.
KW Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT DOMAIN 1 28 Cytoplasmic (Potential).
FT TRANSMEM 29 49 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 50 177 Extracellular (Potential).
FT CARBOHYD 129 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 161 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 177 AA; 20307 MW; 3D78CE6B90F4C9E3 CRC64;

Query Match 100.0%; Score 675; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCAKGPEPSKQMASSEPPCVNKRYSDWKLETLONGLYITIQVAPNANYNDVA 60
DB 52 EIAKEPCAKGPEPSKQMASSEPPCVNKRYSDWKLETLONGLYITIQVAPNANYNDVA 111
QY 61 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDILINSEHQVKNNTYWGIIILA 120
DB 112 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDILINSEHQVKNNTYWGIIILA 171
QY 121 NPQRTS 126
DB 172 NPQRTS 177

RESULT 2
AAH69111 PRELIMINARY; PRT; 177 AA.
AC AAH69111;
DT 24-MAY-2004 (TREMBlrel. 27, Created)
DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein (Fragment).
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=synthetic constructs;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywniak M.I., Skalska U., Smalios D.E., Scherch A., Schein U.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=synthetic constructs;
RA Strausberg R.;
RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC069111; AAH69111.1; -
FT NON TER 1
SQ SEQUENCE 177 AA; 20307 MW; 3D78CE6B90F4C9E3 CRC64;

Query Match 100.0%; Score 675; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCAKGPEPSKQMASSEPPCVNKRYSDWKLETLONGLYITIQVAPNANYNDVA 60
DB 52 EIAKEPCAKGPEPSKQMASSEPPCVNKRYSDWKLETLONGLYITIQVAPNANYNDVA 111
QY 61 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDILINSEHQVKNNTYWGIIILA 120
DB 112 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDILINSEHQVKNNTYWGIIILA 171
QY 121 NPQRTS 126
DB 172 NPQRTS 177

RESULT 3
AAH69319 PRELIMINARY; PRT; 177 AA.
AC AAH69319;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein.
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC069319, AAH69319.1, - 3D78CEB9074C9B3 CRC64;
 SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB9074C9B3 CRC64;

Query Match 100.0%; Score 675; DB 2; Length 177;
 Best local Similarity 100.0%; Pred. No. 1,1e-57;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPEOMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGVAPNANYNDVA 60
 |||||
 DB 52 ETAKPEOMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGVAPNANYNDVA 111
 |||||
 QY 61 PFEVRLYKNDVLTQNLTKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIIL 120
 |||||
 DB 112 PFEVRLYKNDVLTQNLTKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIIL 171
 |||||

QY 121 NPOFIS 126
 |||||
 DB 172 NPOFIS 177

RESULT 4
 ID Q80YG2 PRELIMINARY; PRT; 173 AA.
 AC Q80YG2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE GTR ligand.
 GN Name=Thsf18; Synonyms=tnfsf 18;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/23;
 RA Bianchini R., Nocentini G., Ronchetti S., Ayroldi E., Riccardi C.,
 RL Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/Ca;
 RX PubMed=14608036;
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,
 RA Waldmann H.;
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is
 a costimulatory for T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).

DR EMBL: AY234223; AA089011.1; -
 DR EMBL: AJ577579; CAE12166.1; -
 DR EMBL: AJ577580; CAE12167.1; -
 DR MGI: 2673064; Tnfsf18.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR008983; TNF_1ike.
 DR InterPro: IPR003636; TNF_subf.1.
 DR ProDom: PD002012; TNF_subf.1.
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 51.6%; Score 348; DB 2; Length 173;
 Best Local Similarity 56.7%; Pred. No. 7.5e-26;

Matches 72; Conservative 14; Mismatches 39; Indels 2; Gaps 2;
 QY 2 TAKEPEOMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGVAPNANYNDV 59
 |||||
 DB 47 TAKEPEOMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGVAPNANYNDV 106
 |||||
 QY 60 APEVRLYKNDVLTQNLTKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIIL 119
 |||||
 DB 107 APEVRLYKNDVLTQNLTKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIIL 166
 |||||
 QY 120 ANPOFIS 126
 |||||
 DB 167 PDLPTIS 173

RESULT 5
 ID CAE12166 PRELIMINARY; PRT; 173 AA.
 AC CAE12166;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE GTR ligand.
 GN TNFSF 18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/Ca;
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,
 RA Waldmann H.;
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is
 a costimulatory for T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).
 DR EMBL: AJ577579; CAE12166.1; -
 KW Alternative splicing.
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 51.6%; Score 348; DB 2; Length 173;
 Best Local Similarity 56.7%; Pred. No. 7.5e-26;
 Matches 72; Conservative 14; Mismatches 39; Indels 2; Gaps 2;

QY 2 TAKEPEOMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGVAPNANYNDV 59
 |||||
 DB 47 TAKEPEOMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGVAPNANYNDV 106
 |||||
 QY 60 APEVRLYKNDVLTQNLTKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIIL 119
 |||||
 DB 107 APEVRLYKNDVLTQNLTKSKIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIIL 166
 |||||
 QY 120 ANPOFIS 126
 |||||
 DB 167 PDLPTIS 173

RESULT 6
 ID CAE12167 PRELIMINARY; PRT; 173 AA.
 AC CAE12167;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE GTR ligand.
 GN TNFSF 18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/Ca;

RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,
 RA Waldmann H.,
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is
 RT costimulatory for T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).
 DR EMBL: AJ577580; CAB12167.1; -.
 KW Alternative splicing.
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 51.6%; Score 348; DB 2; Length 173;
 Best Local Similarity 56.7%; Pred. No. 7.5e-26;
 Matches 72; Conservative 14; Mismatches 39; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPLPSKQWMASSPPCVNKVSDMKLEIIQNGLYLYIGVAP-NANY-NDV 59
 DB 47 TAISSCWVKFELSSSKMHMTSPKHCVNTTSDGKLKILQSGTYLYIGVIVPDKRYIKDN 106
 QY 60 APEFVRLYKKNKMTQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIIL 119
 DB 107 APEFVQIYKKNVDVLTLMNDFOILPIGVYELHAGDNILYLFKNSKDHIOKNNYWGIIIL 166
 QY 120 ANPQFIS 126
 DB 167 PDLFFIS 173

RESULT 7
 Q7TNY2 PRELIMINARY; PRT; 173 AA.
 AC Q7TNY2;
 DT 01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, last sequence update)
 DE GTR ligand.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C;
 RX PubMed=14647196;
 RA Kim J.D., Choi B.K., Bae J.S., Jee U.H., Han I.S., Lee H.W.,
 RA Youn B.S., Vinay D.S., Kwon B.S.;
 RT "Cloning and characterization of GTR ligand.";
 RL Genes Immun. 4:564-569(2003).
 DR EMBL: AY267900; AAP6745.1;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR InterPro: IPR003636; TNF subf.
 DR Prodom: PD002012; TNF subf. 1.
 SQ SEQUENCE 173 AA; 19773 MW; 1FD22953BCFC34C5 CRC64;

Query Match 51.0%; Score 344; DB 2; Length 173;
 Best Local Similarity 55.9%; Pred. No. 1.8e-25;
 Matches 71; Conservative 14; Mismatches 40; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPLPSKQWMASSPPCVNKVSDMKLEIIQNGLYLYIGVAP-NANY-NDV 59
 DB 47 TAISSCWVKFELSSSKMHMTSPKHCVNTTSDGKLKILQSGTYLYIGVIVPDKRYIKDN 106
 QY 60 APEFVRLYKKNKMTQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIIL 119
 DB 107 APEFVQIYKKNVDVLTLMNDFOILPIGVYELHAGDNILYLFKNSKDHIOKNNYWGIIIL 166
 QY 120 ANPQFIS 126
 DB 167 PDLFFIS 173

RESULT 8
 Q7TSS5

ID Q7TSS5 PRELIMINARY; PRT; 173 AA.
 AC Q7TSS5;
 DT 01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, last annotation update)
 DE GTR ligand (Glucocorticoid-induced-tumor necrosis factor receptor
 DE ligand).
 GN Name=Gtr1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57/BL6; TISSUE=Spleen;
 RA J. H., Terhorst C.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/O;
 RX MEDLINE=22883945; PubMed=1452128;
 RA Yu K.-Y., Kim H.S., Song S.-Y., Min S.S., Jeong J.J., Youn B.S.;
 RT "Identification of a ligand for glucocorticoid-induced tumor necrosis
 RT factor receptor constitutively expressed in dendritic cells.";
 RL Biochem. Biophys. Res. Commun. 310:433-438(2003).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/J;
 RA Yu K.-Y., Min S.S., Youn B.-S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY320040; AAP70494.1; -.
 DR EMBL: AY359852; AAQ5265.1; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR003636; TNF subf.
 DR Prodom: PD002012; TNF subf. 1.
 KW Receptor.
 SQ SEQUENCE 173 AA; 19732 MW; 0F08494CACF424D2 CRC64;

Query Match 50.7%; Score 342; DB 2; Length 173;
 Best Local Similarity 55.9%; Pred. No. 2.9e-25;
 Matches 71; Conservative 14; Mismatches 40; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPLPSKQWMASSPPCVNKVSDMKLEIIQNGLYLYIGVAP-NANY-NDV 59
 DB 47 TAISSCWVKFELSSSKMHMTSPKHCVNTTSDGKLKILQSGTYLYIGVIVPDKRYIKDN 106
 QY 60 APEFVRLYKKNKMTQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIIL 119
 DB 107 APEFVQIYKKNVDVLTLMNDFOILPIGVYELHAGDNILYLFKNSKDHIOKNNYWGIIIL 166
 QY 120 ANPQFIS 126
 DB 167 PDLFFIS 173

RESULT 9
 AAQ55265 PRELIMINARY; PRT; 173 AA.
 ID AAQ55265;
 DT 02-MAR-2004 (TREMblrel. 27, Created)
 DT 02-MAR-2004 (TREMblrel. 27, last sequence update)
 DT 02-MAR-2004 (TREMblrel. 27, last annotation update)
 DE Glucocorticoid-induced-tumor necrosis factor receptor ligand.
 GN GTR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=129/J;
RX MEDLINE=22883945; PubMed=14521928;
RA Yu K.-Y., Kim H.S., Song S.-Y., Min S.S., Jeong J.J., Youn B.S.;
RT "Identification of a ligand for glucocorticoid-induced tumor necrosis
factor receptor constitutively expressed in dendritic cells.";
RL Biochem. Biophys. Res. Commun. 310:433-438(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RA Yu K.-Y., Min S.S., Youn B.S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; A335952; A305265.1; -.
SQ SEQUENCE 173 AA; 19732 MW; 0F08494CAC424D2 CRC64;

Query Match
Best Local Similarity 55.9%; Pred. No. 2.9e-25;
Matches 71; Conservative 14; Mismatches 40; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPIPSKQMASSPPCVNKNVSDMKLEILQNGLYLTIGQVAP-NANV-NDV 59
Db 47 TATESCMVKEFLSSSKHMTSPKPHCVNTSDGKTLQSGYLTIGQVLPVKKYIKDN 106
QY 60 APPFVPLKKNKMDIQTITNSKIQNVGTYELHVGDTIDLFNSEHQVLKNTYWGIIIL 119
Db 107 APPFVQIYKKNVDVLTQIMNDPQILPIGQVTEHAGDNITYLKNPSKHIOKNTYWGIIIL 166
QY 120 ANPQFIS 126
Db 167 PDLPIFIS 173

RESULT 10
TNFS CHICK STANDARD; PRT; 272 AA.
ID TNFS CHICK STANDARD; PRT; 272 AA.
AC Q918D8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE L) (CD154 protein).
GN Name=TNFSF5; Synonyms=CD40LG, CD40L;
OS Gallus gallus (Chicken);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Spleen;
RA Tregaskes C.A., Young J.R., Burnside J.;
RT "Cloning of a putative chicken CD40 ligand."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell
CC proliferation in the absence of IL-4. Involved in immunoglobulin
CC production in the presence of IL-4.
CC Class switching (By similarity).
CC -|- SUBUNIT: Homotrimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -|- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -|- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ243435; CAB95748.2; -.

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DR HSPB; P29965; 119R.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005174; F:CD40 receptor binding; ISS.
DR GO; GO:0042100; P:B-cell proliferation; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01702; CD40LGAND.
DR ProDom; PD008600; TNF_5; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00469; TNF_2; 1.
KW Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT CHAIN 1 272
FT CHAIN 111 272
FT DOMAIN 1 23
FT TRANSMEM 24 44
FT DOMAIN 45 272
FT SITE 110 111
FT DISUPPID 124 229
FT CARBOHYD 146 146
FT CARBOHYD 251 251
SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;

Query Match
Best Local Similarity 16.1%; Score 108.5; DB 1; Length 272;
Best Local Similarity 29.8%; Pred. No. 0.027;
Matches 36; Conservative 22; Mismatches 44; Indels 19; Gaps 5;

QY 17 KQWMASSPPCVNKNVSDMKLEILQNGLYLTIGQVAPNANVNDVAFPERLY----- 67
Db 153 KM-MTSTYAPLSSLSHYEGKLEKVEKGLYIYSQVSCFCKMAASAFETLYIYLPMEE 211
QY 68 -----KKKMDIQTITNSKIQNV--GGTYELHVGDT--IDLFNSEHQVLKNTYWGIIIL 118
Db 212 DRLMKGLDHTSTALCELQSIREGVFELRQGMVFVNTDSTAVNPNNGNTYFGNFK 271
QY 119 L 119
Db 272 L 272

RESULT 11
ID Q961B8 PRELIMINARY; PRT; 516 AA.
AC Q961B8;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
DE Dictyostelium discoideum (Slime mold).
OS Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafarski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;

```

RA Baumgart C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC116551; AAO52204.1; -
KW Hypothetical protein.
SQ SEQUENCE 516 AA; 58667 MW; 80B308CF6CDF97C2 CRC64;

Query Match 12.8%; Score 86.5; DB 2; Length 516;
Best Local Similarity 29.0%; Pred. No. 7.9;
Matches 27; Conservative 17; Mismatches 36; Indels 13; Gaps 3;

QY 29 NKVSDMKLEILQNGYLYIGQVAPNPNYVAPFEVRLYNKMKMIGTLNKSQIQVGGT 88
DB 419 NKTEDSKLTF-----LYTY-----NIEKQVQPOVTEFETDEINEMITKFOIENNDD 469
QY 89 YELHVGDTIDLIENSEHOVLKNNYWGIIILAN 121
DB 470 VNNINEXKNDIFLN-----IPKQDNCQGIILITN 498

RESULT 12

ID Q896D6 PRELIMINARY; PRT; 270 AA.

AC Q896D6;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Kila protein, putative phage-related DNA binding protein.
GN Name=kila; OrderedLocustNames=CTC01071;
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid=1513;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / B88;
RX MEDLINE=22457253; PubMed=12552129;
RA Bruggemann H., Baumer S., Fricke W.F., Wierzer A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease."
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL: AE015939; AAO35654.1; -
DR InterPro: IPR003497; BRO-N. 1.
DR Pfam: PF02498; Bro-N. 1.
KW Complete proteome.
SQ SEQUENCE 270 AA; 31533 MW; C378AB524C0133A8 CRC64;

Query Match 12.7%; Score 85.5; DB 2; Length 270;
Best Local Similarity 25.4%; Pred. No. 4.7;
Matches 31; Conservative 18; Mismatches 36; Indels 37; Gaps 5;

QY 30 KVSQDKLEILQNGYLYIGQVAPNPNYVAPFEVRLYNKMKMIGTLNKSQIQVGGT 88
DB 134 KAKVMKLEILQNGYLYIGQVAPNPNYVAPFEVRLYNKMKMIGTLNKSQIQVGGT 186
QY 89 -----YELHVG-----DTIDLIENSEHOVLKNNYWGIIILAN 119
DB 187 LNKLLHKLKVOYKQNDQWLTKYKSGKGYTSETIDIVSGSRGPVKNNTKQTKGRFL 246
QY 120 AN 121
DB 247 YN 248

RESULT 13

ID Q81AW5 PRELIMINARY; PRT; 599 AA.

AC Q81AW5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein PF08_0083.

GN Name=PF08_0083;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_Taxid=36329;
RN (1)
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Bartell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL844507; CAD51245.1; -
KW Hypothetical protein.
SQ SEQUENCE 599 AA; 70706 MW; B50A265C5D01AE28 CRC64;

Query Match 12.3%; Score 83; DB 2; Length 599;

Best Local Similarity 22.9%; Pred. No. 21;
Matches 32; Conservative 24; Mismatches 32; Indels 52; Gaps 6;

QY 28 VNKSPDKLEILQNGYLYIGQVAPNPNYVAPFEVRLYNKMKMIGTLNKSQIQVGGT 76
DB 409 KNNMSN--MSNNNNRLLYLKSSSLNNNSPNNIKPLYNQYQSNKNLYTLNHNQNPINQ 466
QY 77 -----TNKSKI-----QVSGTYELHVGDTIDLIENSEHOVLK-- 109
DB 467 KMSFDNNIPSNNKKNYQNNKSTYLLNNLNKNSGSGLLHSGNNMLCYSOQNSLNDM 526
QY 110 -----NNTYWGIIILANPOF 124
DB 527 NREHDNNMY-----NPDF 539

RESULT 14

ID Q8QXN1 PRELIMINARY; PRT; 3063 AA.

AC Q8QXN1;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Sugarcane mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Polyvirus.
OX NCBI_Taxid=12224;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22105130; PubMed=12111432;
RA Chen U., Chen J.P., Adams M.U.;
RT "Characterisation of polyviruses from sugarcane and maize in China."
RL Arch. Virol. 147:1237-1246(2002).
CC -!- SIMILARITY: Belongs to the polyviruses polyprotein family.
DR EMBL: AJ101015; CAC84095.1; -
DR HSSP: P04517; ILVM.
DR MEROPS: C06.001; -.

DR GO:GO:0019028; C:viral capsid; IEA.
DR GO:GO:0005524; F:ATP binding; IEA.
DR GO:GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO:GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO:GO:0003723; F:RNA binding; IEA.
DR GO:GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO:GO:0006508; F:structural molecule activity; IEA.
DR GO:GO:0006350; P:translation; IEA.
DR GO:GO:0019079; P:viral genome replication; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR011545; DEAD/DEAH N.
DR InterPro: IPR001650; Helicase C.
DR InterPro: IPR001730; Peptidase C4.
DR InterPro: IPR001456; peptidase_C6.
DR InterPro: IPR002540; pept_S30_Poly_P1.
DR InterPro: IPR001592; Poly_coat.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_Psv1r.

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DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00851; Peptidase_C6; 1.
DR Pfam; PF00767; Polypeptidase; 1.
DR Pfam; PF01577; Poly P1; 1.
DR Pfam; PF00680; RNA-dep RNA pol; 1.
DR PRINTS; PR00966; NIAOTYPTASE.
DR SMART; SMO0487; DEXDC; 1.
DR SMART; SMO0490; HELIC; 1.
DR ATP-binding; Coat protein; Helicase; Hydrolase; Polypeptidase.
FT CHAIN 694 1040
FT CHAIN 1041 1107
FT CHAIN 1108 1745
FT CHAIN 1746 1798
FT CHAIN 1799 1987
FT CHAIN 1988 2229
FT CHAIN 2 233
FT CHAIN 2230 2750
FT CHAIN 2751 3063
FT CHAIN 3063 693
FT CHAIN 3063 693
SQ SEQUENCE 3063 AA; 346241 MW; E6019C8D1E80B59D CRC64;

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Query Match 12.3%; Score 83; DB 2; Length 3063;
Best local similarity 29.2%; Pred. No. 1.4e+02;
Matches 35; Conservative 15; Mismatches 50; Indels 20; Gaps 5;

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QY 4 KEPCKAKGFLPSSKQWASSPPCVNKSVDWKLFIQNGLYTIGQVAPNPNYDVAFPE 63
DB 338 KERNCPFTSHPLMQVAFETIGHTDNGSKOILDI-SALALKVITLPDDVAKASVALL 396
QY 64 V-RLYKXK-----DMIGTLTKSKIQWGGTYELHVGDTIDLIENSEHOVLKKN-NTYWG 115
DB 397 VSRWYKXKRESLKTDLTETFPNKKVSPKS-----TINAAIMCNDLKNANFVWG 445

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RESULT 15

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ID Q6HHW4 PRELIMINARY; PRT; 459 AA.
AC Q6HHW4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Dihydroliopamide dehydrogenase (EC 1.8.1.4).
GN Name=acdl; ORFNames=B19727.2536;
OS Bacillus thuringiensis serovar konkukian str. 97-27.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus thuringiensis serovar konkukian.
OX NCBI_TaxID=281309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka K.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Protein N(6)-(dihydroliopoyl) lysine + NAD(+) =
CC protein N(6)-(lipoyl) lysine + NADH.
CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -1- MISCELLANEOUS: The active site is a redox-active disulfide bond
CC (By similarity).
CC -1- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
CC oxidoreductase family.
CC EMBL; AE017355; AAT61350.1; -.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR000815; Hg_reductase.
DR InterPro; IPR006258; Lipamide_dh.
DR InterPro; IPR000205; NAD_BS.
DR InterPro; IPR000103; Pyridine_redox_2.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR004099; Pyr_redox_dim.
DR Pfam; PF00070; Pyr_redox; 1.

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DR Pfam; PF02852; Pyr_redox_dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00945; HGRDTASE.
DR PRINTS; PR00411; PNDRDTASEII.
DR PRINTS; PR00469; PNDRDTASEII.
DR ProDom; PD000139; FAD_pyr_redox; 1.
DR TIGRFAMs; TIGR01350; Lipamide DH; 1.
DR PROSITE; PS00076; PYRIDINE_REDOX_1; UNKNOWN 1.
DR FAD; Flavoprotein; NAD; Oxidoreductase; Redox-active center.
SQ SEQUENCE 459 AA; 49338 MW; B9F88C0FC93DD331 CRC64;

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Query Match 11.8%; Score 79.5; DB 2; Length 459;
Best local similarity 25.4%; Pred. No. 33;
Matches 32; Conservative 25; Mismatches 56; Indels 13; Gaps 6;

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QY 5 EPCMAKFGPLPSKQWASSPPCVNKSVDWKLFIQNGLY-----LIYGVAAPNPNYDV 59
DB 144 EPAPLPAPDPGKWLINSSHAMSLNIPK-SLLVGGGVIGCEFAISYISRLGTVTIEM 202
QY 60 APFEVRLVKNKDMIGTLTKSKIQWGGTYELHVGDTIDLIENSEHOVLKKNNTYWGILL 119
DB 203 AP-QLLPGEEDIDQIL--KEKESDG--VEIFGAALKGLNRYKKA--SFYKGSIQE 255
QY 120 ANPQFI 125
DB 256 ANPEYV 261

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Search completed: November 2, 2004, 12:58:45
Job time : 194 secs

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